

WO 03/072719

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PCT/US03/05271

NL/4/01 (B)	AACAGACAGA	CCACCCAAAC	AACCGCAGAG	AAAAAGCCAA	CCAGAGCAAC	AACCAAAA--
UK/5/01 (B)	AACAGACAGA	CCACCCAAAC	AACTGCAGAG	AAAAAGCCAA	CCAGAGCAAC	AACCAAAA--

	485	495	505	515	525	535
NL/1/00 (p)	-----	-AACACATTC	TCCACCACGG	GCAACGACAA	GGACGGC--A	CGCAG-AACC
BR/2/01 (A)	-----	-AACACATTC	TCCACCACGG	GCAACGACAA	GGACGGC--A	CGCAGGAACC
FL/4/01 (A)	-----	-AACACACTC	TCCACCATGG	GCAACGACAA	GGACGGC--A	CGCAG-AACC
FL/3/01 (A)	-----	-AACACATTC	TCCACCATGG	GCAACGACAA	GGACGGC--A	CGCAG-AACC
FL/8/01 (A)	-----	-AACACATTC	TCCACCATGG	GCAACGACAA	GGACGGC--A	CGCAG-AACC
FL/10/01 (-----	-AACACATTC	CCCACCATGG	GCAATGACAA	GGACGGT--C	CGCGG-AACC
NL/10/01 (-----	-AACACATTC	CCCACCATGG	GCAATGACAA	GGACGGT--C	CGTGG-AACC
NL/2/02 (A)	-----	-AACACATTC	CCCACCATGG	GCAATGACAA	GGACGGT--C	CGTGG-AACC
NL/17/00 (-----	-TACACAATC	CCCACCACGG	ACAACAACGA	AGGCAAT--C	CGCAG-AGCC
NL/1/81 (A)	-----	-AACACAATC	CCCACCACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGCC
NL/1/93 (A)	-----	-AACACAATC	CCCACCACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGAC
NL/2/93 (A)	-----	-AACACAATC	ACCACCACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGAC
NL/3/93 (A)	-----	-AACACAATC	CTCAATACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGCC
NL/1/95 (A)	-----	-AACACAATC	CCCACCACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGCC
NL/2/96 (A)	-----	-CACACAATC	CCCACCACGG	GTAACAACGA	AGGCAAT--C	CTCAG-AGCC
NL/3/96 (A)	-----	-AACACAATC	CCCACCACGG	GCAACAACGA	AGGCGGT--C	CTCAG-AGCC
NL/22/01 (-----	-AACACAGTC	CCCACCACGG	ACAACAGCGA	AGGCGGT--C	CCCAG-AGCC
NL/24/01 (-----	-AACACAGTC	CCCACCACGG	ACAACAGCGA	AGGCGGT--C	CCCAG-AGCC
NL/23/01 (-----	-AACACAGTC	CCCACCACGG	ACAACAGCGA	AGGCGGT--C	CCCAG-AGCC
NL/29/01 (-----	-TACACAATC	CCCACCACGG	GCAACAACGA	AGGCAAT--C	CGCAG-AGCC
NL/3/02 (A)	-----	-TACACAATC	CCCACCACGG	GCAACAACGA	AGGCAAT--C	CGCAG-AGCC
NL/1/99 (p)	AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGCAAC	CCAAACAACC
NL/11/00 (AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGCAAC	CCAAACAACC
NL/12/00 (AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGTAC	CCAAACAACC
NL/5/01 (B)	AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGCAAC	CCAAACAACC
NL/9/01 (B)	AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGCAAC	CCAAACAACC
NL/21/01 (AGGGAAAAAG	GAAAAGAAAA	CACAAACCAA	ACCACAAGCA	CAGCTGCAAC	CCAAACAACC
NL/1/94 (p)	-----	---AAGAAAC	CACAACCTCGA	ACTACAAGCA	CAGCTGCAAC	CCAAACACTC
NL/1/82 (B)	-----	---AAGAAAC	CACAACCTCGA	ACTACAAGCA	CAGCTGCAAC	CCAAACACTC
NL/1/96 (B)	-----	---AAGAAAC	CACAACCTCGA	ACTACAAGCA	CAGCTGCAAC	CCAAACACTC
NL/6/97 (B)	-----	---AAGAAAC	CACAACCTCGA	ACTACAAGTA	CAGCTGCAAC	CCAAACACCC
NL/9/00 (B)	-----	---AAGAAAC	CACAACCTCGA	ACCACAAGCA	CAGCTGCAAC	CCAAACACTC
NL/3/01 (B)	-----	---AAGAAAC	CATAACTCGA	ACCACAAGCA	CAGCCGCAAC	CCAAACACTC
NL/4/01 (B)	-----	---AAGAAAC	CATAACTCGA	ACCACAAGCA	CAGCTGCAAC	CCAAACACTC
UK/5/01 (B)	-----	---AAGAAAC	CACAACCTCGA	ACCACAAGCA	CAGCTGCAAC	CCAAACACTC

	545	555	565	575	585	595
NL/1/00 (p)	ACCACTCTCC	GCACAAGCAG	CACAAGAAAG	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
BR/2/01 (A)	ACCACTCTCC	GCACAAGCAG	CACAAGAAAG	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
FL/4/01 (A)	ACCACTCTCC	GCACAAGCAG	CACAAGAAAG	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
FL/3/01 (A)	ACCACTCTCC	GCACAAGCAG	CACAAGAAAG	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
FL/8/01 (A)	ACCACTCTCC	GCACAAGCAG	CACAAGAAAG	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
FL/10/01 (ACCACTCTCC	GCACAAGCAG	CACAAGAAAA	AGACTGTCTA	CAGCATCAGT	CCAACCTGAC
NL/10/01 (ACCACTCTCC	GCACAAGCAG	CATAAGAAAA	AGACCGTCCA	CAGCATCAGT	CCAACCTGAC
NL/17/00 (ACCACTTTCC	GCATGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATTAGT	CCAGTCCGAC
NL/1/81 (A)	ACCGCTTTCC	GCACGAGCAG	CACAAGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/1/93 (A)	ACCGCTTTCC	ACACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/2/93 (A)	ACCGCTTTCC	ACACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/3/93 (A)	ACCGCTTTCC	GCACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/1/95 (A)	ACCGCTTTCC	GCACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/2/96 (A)	ACCGCTTTCC	GCATGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATTAGT	CCAGTCCGAC
NL/3/96 (A)	ACCGCTTTCC	GCATGAGCAG	CACAGGAAAA	AGACCAACCA	CAACATCAGT	CCAGTCTGAC
NL/24/01 (ACCGCTTTCC	GCACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACACAGT	CCAGCCGAT
NL/24/01 (ACCGCTTTCC	GCACGAGCAG	CACAGGAAAA	AGACCAACCA	CAACACAGT	CCAGCCGAT

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NL/23/01 (ACCGCCCTTC	GCACGAGCAG	CACAGGAGAA	AGACCAACCA	CAACACCAGT	CCAGCCCGAT
NL/29/01 (ACCACCCTCC	GCATGAGCAG	CACAGGAAGA	AGACCAACCA	CAACACTAGT	CCAGTCCGAC
NL/3/02 (A	ACCACCCTCC	GCATGAGCAG	CACAGGAAGA	AGACCAACCA	CAACACTAGT	CCAGTCCGAC
NL/1/99 (p	AACACCACCA	ACCAAATCAG	AAATGCAAGT	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/11/00 (AACACCACCA	ACCAAATCAG	AAATGCAAGT	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/12/00 (AACACCACCA	ACCAAATCAG	AAATGCAAGC	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/5/01 (B	AACACCACCA	ACCAAATCAG	AAATGCAAGC	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/9/01 (B	AACACCACCA	ACCAAATCAG	AAATGCAAGC	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/21/01 (AACACCACCA	ACCAAATCAG	AAATGCAATT	GAGACAATCA	CAACATCCGA	CAGACCCAGA
NL/1/94 (p	AACACTACCA	ACCAAATCAG	CTATGTGAGA	GAGGCAACCA	CAACATCCGC	CAGATCCAGA
NL/1/82 (B	AACACCACCA	ATCAAACCAG	AAATGGAAGA	GAGACAACCA	TAACATCTGC	CAGATCCAGA
NL/1/96 (B	AACACCACCA	ACCAAATCAG	CAATGGAAGA	GAGGCAACCA	CAACATCCAC	CAGATCCAGA
NL/6/97 (B	AACACCACCA	ACCAAACCAG	CAATGGAAGA	GAGGCAACCA	CAACATCCGC	CAGGTCCAGA
NL/9/00 (B	AACACCACCA	ACCAAATCAG	CAATGGAAGA	GAGGCAACCA	CAACATCTGC	CAGATCCAGA
NL/3/01 (B	AACACCACCA	ACCAAACCAG	CAATGGAAGA	GAGGCAACCA	CAACATCTGC	CAGATCCAGA
NL/4/01 (B	AACACCACCA	ACCAAACCAG	CAATGGAAGA	GAGGCAACCA	CAACATCTGC	CAGATCCAGA
UK/5/01 (B	AACACCACCA	ACCAAATCAG	CAATGGAAGA	GAGGCAACCA	CAACATCTGC	CAGATCCAGA

	605	615	625	635	645	655
NL/1/00 (p	ATCAGCGCAA	CAACCCACAA	AAACGAAGAA	GCAAGTCCAG	CGAGCCCACA	AACATCTGCA
BR/2/01 (A	ATCAGCGCAA	CAACCCACAA	AAACGAAGAA	GCAAGTCCAG	CGAGCCCACA	AACATCTGCA
FL/4/01 (A	ATCAGCGCAA	CAACCCACAA	AAACGAAGAA	GCAAGTCCAG	CGAGCCCACA	AACATCTGCA
FL/3/01 (A	ATCAGCGCAA	CAACCCACAA	AAACGAAGAA	GCAAGTCCAG	CGAGCCCACA	AACATCTGCA
FL/8/01 (A	ATCAGCGCAA	CAACCCACAA	AAACGAAGAA	GCAAGTCCAG	CGAGCCCACA	AACATCTGCA
FL/10/01 (AGCAGCGCAA	CAACCCACAA	ACACGAAGAA	ACAAGCCCAG	TGAGCCCACA	AACATCTGCA
NL/10/01 (AGCAGCGCAA	CAACCCACAA	ACACGAAGAA	GCAAGCCCAG	TGAGCCCACA	AGCATCTGCA
NL/2/02 (A	AGCAGCGCAA	CAACCCACAA	ACACGAAGAA	GCAAGCCCAG	TGAGCCCACA	AGCATCTGCA
NL/17/00 (AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGTTTCAG	CGAAGCCCACA	GGCGTCTGCA
NL/1/81 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAAGTTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/1/93 (A	AGCAGCACCA	CAACTCAAAA	TCATGAAGAA	ACAAGTTTCAT	CGAAGCCCACA	GGCATCTGCA
NL/2/93 (A	AGCAGCACCA	CAACTCAAAA	TCATGAAGAA	ACAAGTTTCAT	CGAAGCCCACA	GGCATCTGCA
NL/3/93 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGTTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/1/95 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGTTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/2/96 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGTTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/3/96 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGTTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/22/01 (AGCAGCACCA	CAACACAAAA	TCATGAAGAA	ACAGGCTTCAG	CGAAGCCCACA	GGCATCCGCA
NL/24/01 (AGCAGCACCA	CAACACAAAA	TCATGAAGAA	ACAGGCTTCAG	CGAAGCCCACA	GGCATCCGCA
NL/23/01 (AGCAGCACCA	CAACACAAAA	TCATGAAGAA	ACAGGCTTCAG	CGAAGCCCACA	GGCATCCGCA
NL/29/01 (AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGCTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/3/02 (A	AGCAGCACCA	CAACCCAAAA	TCATGAAGAA	ACAGGCTTCAG	CGAAGCCCACA	GGCATCTGCA
NL/1/99 (p	ACTGACACCA	CAACCCAAAG	CAGCGAACAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/11/00 (ATTGACACCA	CAACCCAAAG	CAGCGATCAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/12/00 (ACTGACTCCA	CAACCCAAAG	CAGCGAACAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/5/01 (B	ACTGACTCCA	CAACCCAAAG	CAGCGAACAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/9/01 (B	ACTGACTCCA	CAACCCAAAG	CAGCGAACAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/21/01 (ACTGACTCCA	CAACCCAAAG	CAGCGAACAG	ACAA-CCCGG	GCAACAGACC	CAAGCTCCCC
NL/1/94 (p	AACAGTGCCA	CAACTCAAAG	CAGCGACCAA	ACAA-CCCGG	GCAGCAGACC	CAAGCTCCCC
NL/1/82 (B	AACGAGGCCA	CAACTCAAAG	CAGCGAACAA	ACAA-ACCAG	ACAACAGACC	CAAGCTCCCC
NL/1/96 (B	AACGGTGCCA	CAACTCAAAG	CAGCGATCAA	ACAA-CCTAG	ACAGCAGACC	CAAGCTCCCC
NL/6/97 (B	AACGGTGCCA	CAACTCAAAG	CAGCGATCAA	ATAA-CCAG	GCAGCAGACC	CAAGCTCCCC
NL/9/00 (B	AACAATGCCA	CAACTCAAAG	CAGCGATCAA	ACAA-CCCGG	GCAGCAGACC	CAAGCTCCCC
NL/3/01 (B	AACAATGCCA	CAACTCAAAG	CAGCGACCAA	ACAA-CCCGG	GCAGCAGACC	CAAGCTCCCC
NL/4/01 (B	AACAATGCCA	CAACTCAAAG	CAGCGACCAA	ACAA-CCCGG	GCAGCAGACC	CAAGCTCCCC
UK/5/01 (B	AACAATGCCA	CAACTCAAAG	CAGCGATCAA	ACAA-CCCAA	GCAGCAGAAC	CAAACTCCCC

	665	675	685	695	705	715
NL/1/00 (p	AGCACAAACAA	GAATACAAAG	GAAAAGCGTG	GAGGCCAACA	CATCAACAAC	ATACAACCAA
BR/2/01 (A	AGCACAAACAA	GAATACAAAG	GAAAAGCGTG	GAGGCCAACA	CATCAACAAC	ATACAACCAA
FL/4/01 (A	AGCACAAACAA	GAATACAAAG	GAAAAGCGTG	GAGGCCAACA	CATCAACAAC	ATACAACCAA

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FL/3/01 (A -	AGCACAACAA	GAACACAAAG	GAAAAGCGTG	GAGGCCAACA	CATCAACAAC	ATACAACCAA
FL/8/01 (A	AGCACAACAA	GAACACAAAG	GAAAAGCGTG	GAGGCCAACA	CATCAACAAC	ATACAACCAA
FL/10/01 (AGCACAGCAA	GACCACAAAG	GAAGGGCATG	GAGGCCAGCA	CATCAACAAC	ATACAACCAA
NL/10/01 (AGCACAGCAA	GACCACAAAG	GAAGGGCATG	GAGGCCAGCA	CATCAACAAC	ATACAACCAA
NL/2/02 (A	AGCACAGCAA	GACCACAAAG	GAAGGGCATG	GAGGCCAGCA	CATCAACAAC	ATACAACCAA
NL/17/00 (AGCACAATG-	-----CAAAA	-----	-----CTAGCA	CACCAATAAT	ATAAAACCAA
NL/1/81 (A	AGCACAATG-	-----CAAGG	-----	-----CCAGCA	CACCAACAAC	ATAAAACCAA
NL/1/93 (A	AGCACAATG-	-----CAAGA	-----	-----CCAGGA	CACCAACAAT	ACAAAACCAA
NL/2/93 (A	AGCACAATG-	-----CAAGA	-----	-----CCAGGA	CACCAACAAT	ACAAAACCAA
NL/3/93 (A	AGCACAATG-	-----CAAAA	-----	-----CTAGCA	CACCAACATT	GTAAAACCAA
NL/1/95 (A	AGCACAATG-	-----CAAAA	-----	-----CTAGCA	CACCAACATT	GTAAAACCAA
NL/2/96 (A	AGCACAATG-	-----CAAAA	-----	-----CTAGCA	CTCCAACAAT	ATAAAACCAA
NL/3/96 (A	AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACATT	GCAAAAACCAA
NL/22/01 (AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACATT	GCAAGACCAA
NL/24/01 (AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACATT	GCAAGACCAA
NL/23/01 (AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACATT	GCAAGACCAA
NL/29/01 (AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACAAT	ATAAAACCAA
NL/3/02 (A	AGCACAATG-	-----CAAAA	-----	-----CCAGCA	CACCAACAAT	ATAAAACCAA
NL/1/99 (p	ACCACACCAT	GCATAGAGAG	GTGCA-----	-AAACTCAAA	TGAGCACAAC	ACACAAACAT
NL/11/00 (ACCACACCAT	GCACAGAGTG	GTGCA-----	-AAACCCAAA	TGAACACAAC	ACACAAACAT
NL/12/00 (ACCACATCAT	GCACAGGGAA	GTGCA-----	-AAACCCAAA	TGAACACAAC	ACACAAACAT
NL/5/01 (B	AGCACACCAT	GCACAGGGAA	GTGCA-----	-AAACCCAAA	TGAACACAAC	ACACAAACAT
NL/9/01 (B	ACCACACCAT	GCACAGGGAA	GTGCA-----	-AAACCCAAA	TGAACACAAC	ACACAAACAT
NL/21/01 (CCCACACCAT	GCACAGGGAA	GTGCA-----	-AAACCCAAA	TGAACACAAC	ACACAAACAT
NL/1/94 (p	ACCACACCAT	ACACAGAAAA	GCACA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT
NL/1/82 (B	ACCACATCAT	GCATAGATAA	GCACA-----	-ATAACAATA	TGAACACAAC	ACAGACACAT
NL/1/96 (B	ACCACACCAT	ACACAGAAAA	GCACA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT
NL/6/97 (B	ACCACACCAT	ACACAGAAAA	GCACA-----	-ACAACAGCA	T-----ACAAC	ACAGACACAT
NL/9/00 (B	ATCACAACAT	ACACAGAAAA	GCACA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT
NL/3/01 (B	ATCACAACAT	ACACAGAAAA	GCATA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT
NL/4/01 (B	ATCACAACAT	ACAAAGAAAA	GCACA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT
UK/5/01 (B	ATCACAACAT	ACACAGAAAA	GCACA-----	-ACAACAACA	T-----ACAAC	ACAGACACAT

	725	735	745	755	765	775
NL/1/00 (p	ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGCAGACAC	CAACAATGGA
BR/2/01 (A	ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGCAGACAC	CAACAATGGA
FL/4/01 (A	ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGCAGACAC	CAACAATGGA
FL/3/01 (A	ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGCAGACAC	CAACAATGGA
FL/8/01 (A	ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGCAGACAC	CAACAATGGA
FL/10/01 (ACTAGTTAAC	AAAAAATACA	AAATAACTCT	AAGATAAACC	ATGTAGACAC	CAACAATTGA
NL/10/01 (ACTAGTTAAC	AAAAAATATA	AAATAACTCT	AAGATAAACC	ATGTAGACAC	CAACAATTGA
NL/2/02 (A	ACTAGTTAAC	AAAAAATATA	CAATAACTCT	AAGATAAACC	ATGTAGGTAC	CAACAATCAA
NL/17/00 (ATTAGTTAAC	AAAAAATGCG	AGATAGCTCT	AAAGTAAAC	ATGTAGGTAC	CAACAATCAA
NL/1/81 (A	ATTAGTTAAC	AAAAAATACG	AGATAGCTCT	AAAGTAAAC	ATGTAGGTAC	CAACAATCAA
NL/1/93 (A	ATTAGTTAAC	AAAAAATACA	AGATAGCTCT	AAAGTAAAC	ATGTAGGTAC	CAACAGTAAA
NL/2/93 (A	ATTAGTTAAC	AAAAAATACA	AGATAGCTCT	AAAGTAAAC	ATGTAGGTAC	CAACAGTAAA
NL/3/93 (A	ATTAGTTAAC	AAAAAATATG	AAATAGCTCT	AAAGTAAAC	ATGTAGGTGC	TAACAATCAA
NL/1/95 (A	ATTAGTTAAC	AAAAAATATG	AAATAGTTCT	AAAGTAAAC	ATGTAGGTGC	TAACAATCAA
NL/2/96 (A	ATTAGTTAAC	AAAAAATACG	AGATAGCTCT	AAAGTAAAC	ATGTAGGCAC	CAACAATCAG
NL/3/96 (A	ATTAGTTAAC	AAAAAATATG	AAATAGTTCT	AAAGTAAAC	ATGTAGGTGC	CAACAATCAA
NL/22/01 (ATTAGTTAAC	AAAAAATATG	AAATAGCTCT	AAAGTAAAC	ATGTAGGTGC	CAACAATCAA
NL/24/01 (ATTAGTTAAC	AAAAAATATG	AAATAGCTCT	AAAGTAAAC	ATGTAGGTGC	CAACAATCAA
NL/23/01 (ATTAGTTAAC	AAAAAATATG	AAATAGCTCT	AAAGTAAAC	ATGTAGGTGC	CAACAATCAA
NL/29/01 (ATTAGTTAAC	AAAAAATACG	AGATAGCTCT	AAAGTAAAC	ATGTAGGCAC	CAACAATCAA
NL/3/02 (A	ATTAGTTAAC	AAAAAATACG	AGATAGCTCT	AAAGTAAAC	ATGTAGGCAC	CAACAATCAA
NL/1/99 (p	CCCATCCAAG	TAGTTA-ACA	AAAAA-CCAC	AAAAATAA-CC	TTGAAAAC-C	AAAAAA--CC
NL/11/00 (CTCATCCAAG	TAGTTA-ACA	AAAAA-CCAC	AAAAATAA-CC	TTGAAAAC-C	AAAAAA--CC
NL/12/00 (CCCATCCAAG	TAGTTA-ACA	AAAAA-----	-----	-----	-----
NL/5/01 (B	CCCATCCAAG	TAGTTA-ACA	AAAAA-A---	-----	-----	-----
NL/9/01 (B	CCCATCCAAG	TAGTTA-ACA	AAAAA-----	-----	-----	-----

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NL/21/01 (CCCCATCCAAG	TAGTTA-ACA	AAAAA-----	-----	-----	-----
NL/1/94 (p	CCTCTCCAAG	TAGTTA-ACA	AAAAAACTAT	AAAATAA-TC	ATGAAAAC-C	GAAAAA-CTA
NL/1/82 (B	CTTCTCCAAG	TAGTTA-ACA	AAAAA-CTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAA-CTA
NL/1/96 (B	CTTCTCCAAG	TAGTTA-ACA	AAAAA-CTAT	AAAATAA-CC	ATGAAAAC-T	AAAAAA-CTA
NL/6/97 (B	CTTTTCCAAG	TAGTTA-ACA	AAAAA-CTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAA-CTA
NL/9/00 (B	CTTCTCTAAG	TAGTTA-ACA	AAAAAACTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAA-CTA
NL/3/01 (B	CTTCTCCAAG	TAGTTA-ACA	AAAAAACTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAACTA
NL/4/01 (B	CTTCTCCAAG	TAGTTA-ACA	AAAAAACTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAACTA
UK/5/01 (B	CTTCTCTAAG	TAGTTA-ACA	AAAAAACTAT	AAAATAA-CC	ATGAAAAC-C	AAAAAA-CTA

	785	795	805	815	825	835
NL/1/00 (p	GAAGCCAAAA	GACAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCTG
BR/2/01 (A	GAAGCCAAAA	GACAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCTG
FL/4/01 (A	GAAGTCAAAA	GACAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCTG
FL/3/01 (A	GAAGTCAAAA	GACAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCTG
FL/8/01 (A	GAAGTCAAAA	GACAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCTG
FL/10/01 (GAAGCCAAAA	GGCAATTCAC	AATCTCCC-A	AAAAGCAAC	AACACCATAT	TAGC--TCCG
NL/10/01 (GAAGCCAAAA	GGCAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCCG
NL/2/02 (A	GAAGCCAAAA	GGCAATTCAC	AATCTCCCCA	AAAAGGCAAC	AACACCATAT	TAGC--TCCG
NL/17/00 (GAAACCAAAA	GACAATTCAC	AATCTCCCTA	AAACAGCAAC	GACACCATGT	CAGC--TTTG
NL/1/81 (A	GGAATCAAAA	GACAATTCAC	AATCTCCCTA	AAACAGCAAC	AACATCATGT	CAGT--TTTG
NL/1/93 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/2/93 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/3/93 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/1/95 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/2/96 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/3/96 (A	GAAATCAAAA	GACAATTCAC	AATCTCCCCA	AAACAGCAAC	AACATCATGT	CAGC--TTTG
NL/22/01 (GAAATCAAAA	GATAACTCAT	AATCTCTCTA	AAACATCAAC	AACATCATGT	TAAC--TTTG
NL/24/01 (GAAATCAAAA	GATAACTCAT	AATCTCTCTA	AAACATCAAC	AACATCATGT	TAAC--TTTG
NL/23/01 (GAAATCAAAA	GATAACTCAT	AATCTCTCTA	AAACATCAAC	AACATCATGT	TAAC--TTTG
NL/29/01 (GAAACCAAAA	GATAACTCAT	AATCCCCCCA	AAACAGCAAC	GACACCATGT	CAGC--TTTG
NL/3/02 (A	GAAACCAAAA	GATAACTCAT	AATCCCCCCA	AAACAGCAAC	GACACCATGT	CAGC--TTTG
NL/1/99 (p	A-----AAAC	ATAAACCCAG	A---CCCAGA	AA--AACATA	GACACCATAT	GGAAGGTTCT
NL/11/00 (A-----AACC	ACAAACTTAG	A---CCCAGA	AA--AACATA	GACACTATAT	GGAAGGTTTG
NL/12/00 (-----TCAG	A---CCCAGA	AA--AACATA	GACACTATAT	GGAAGGTCCG	
NL/5/01 (B	-----TCAG	A---CCCAGA	AA--AACATA	GACACTATAT	GGAAGGTCCG	
NL/9/01 (B	-----TCAG	A---CCCAGA	AA--AACATA	GACACTATAT	GGAAGGTCCG	
NL/21/01 (-----TCAG	A---CCCAGA	AA--AACATA	GACACTATAT	GGAAGGTCCG	
NL/1/94 (p	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/1/82 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/1/96 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/6/97 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/9/00 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/3/01 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
NL/4/01 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAAGAACACA	AACACTATAT	GAATTGTTTG
UK/5/01 (B	G-----AAAA	GTTAATTTGA	A---CTCAGA	AAGGAACACA	AACACTATAT	GAATTGTTTG

	845	855	865	875	885	895
NL/1/00 (p	CCCAAATCTC	CCTGGAAAAA	AACACTCGCC	CATATACCAA	AAATACCACA	ACCACCCCAA
BR/2/01 (A	CCCAAATCTC	CCTGGAAAAA	AACACTCGCC	CATATACCAA	AAATACCACA	ACCACCCCAA
FL/4/01 (A	CCCAAATCTC	CCTGGAAAAA	AACACTCGCC	CATATACCAA	AAATACCACA	ACCACCCCAA
FL/3/01 (A	CCCAAATCTC	CCTGGAAAAA	AACACTCGCC	CATATACCAA	AAATACCACA	ACCACCCCAA
FL/8/01 (A	CCCAAATCTC	CCTGGAAAAA	AACACTCGCC	CATATACCAA	AAATACCACA	ACCACCCCAA
FL/10/01 (CTTAAATCTC	CCTGAAAAA	AACACTCGCC	CATATACCAA	CTATACCACA	ACCATCCCAA
NL/10/01 (CTTAAATCTC	CCTGAAAAA	AACACTCGCC	CATATACCAA	CTATACCACA	ACCATCCCAA
NL/2/02 (A	CTTAAATCTC	CCTGAAAAA	AACACTCGCC	CATATACCAA	CTATACCACA	ACCATCCCAA
NL/17/00 (CTCAAATCTC	TCTGGGAGA	AACCTTCTACC	CACATACTAA	CAACATCACA	ACCATCTCAA
NL/1/81 (A	CTCAAATCTC	TCTGGGAGA	AACCTTCTACC	CACATACTAA	CAACATCACA	ACCATCTCAA
NL/1/93 (A	CTCAAATCTC	TCTGGGAGA	AACCTTCTACC	CACATACTAA	CAACATCACA	ACTATCTCAA

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NL/2/93 (A)	CTCAAATCTC	CCTGGGAGA-	AACCTCTCGCC	CACATACTAA	CAACATCACA	ACTATCTCAA
NL/3/93 (A)	CTCAAATCTC	CCTGGGAGA-	AACCTTTCGCC	CCCATACTGA	CAACATCACA	ATCATCTCAA
NL/1/95 (A)	CTCAAATCTC	CCTGGGAGA-	AACCTTTCGCC	CCCATACTGA	CAACATCACA	ATCATCTCAA
NL/2/96 (A)	CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CACATACTAA	CAACATCACA	ATCATCTCAA
NL/3/96 (A)	CTCAAATCTC	CCTGGGAGA-	AACCTTTCGCC	CCCATACTGA	CAACATCACA	ATCATCTCAA
NL/22/01 (CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CCCATACTGG	CAACATCACA	ATCATCTCAA
NL/24/01 (CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CCCATACTGG	CAACATCACA	ATCATCTCAA
NL/23/01 (CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CCCATACTGG	CAACATCACA	ATCATCTCAA
NL/29/01 (CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CACATACTAA	CAACATCACA	ACCATCTCAA
NL/3/02 (A)	CTCAAATCTC	TCTGGGAGA-	AACCTTTCGCC	CACATACTAA	CAACATCACA	ACCATCTCAA
NL/1/99 (p)	AGCATATGCA	CCAATGAGAT	GGCATCTGTT	CATGTATCAA	TAGCACCACC	ATTAT-TTAA
NL/11/00 (AGCATATGCA	CCAATGAGAT	GGTATCTGTT	CATGTATCAA	TAGCGCCACC	ATTAT-TTAA
NL/12/00 (AGCATATGCA	CCGATGAAAT	GGCATTTGTT	CATGTATCAA	TAGCGCCACC	ATTAT-TTAA
NL/5/01 (B)	AGCATATGCA	CCGATGAAAT	GGCATCTGTT	CATGTATCAA	TAGCACCACC	ATTAT-TTAA
NL/9/01 (B)	AGCATATGCA	CCGATGAAAT	GGCATCTGTT	CATGTATCAA	TAGCGCCACC	ATTAT-TTAA
NL/21/01 (AGCATATGCA	CCGATGAAAT	GGCATCTGTT	CATGTATCAA	TAGCGCCACC	ATTAT-TTAA
NL/1/94 (p)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
NL/1/82 (B)	AGCATATATA	CTAATGAAAT	AGCATCTGTT	CATGCATCAA	TAATACCATC	ATTAT-TTAA
NL/1/96 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
NL/6/97 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
NL/9/00 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
NL/3/01 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
NL/4/01 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA
UK/5/01 (B)	AGCGTATATA	CTAATGAAAT	AGCATCTGTT	TGTGCATCAA	TAATACCATC	ATTAT-TTAA

	905	915	925
NL/1/00 (p)	GAAAAAAA-C	TGGGCAAAAC	AACACCCAA
BR/2/01 (A)	GAAAAAAA-C	TGGGCAAAAC	AACACCCAA
FL/4/01 (A)	GAAAAAAA-C	TGGGCAAAAC	AACACCCAA
FL/3/01 (A)	GAAAAAAA-C	TGGGCAAAAC	AACACCCAA
FL/8/01 (A)	GAAAAAAA-C	TGGGCAAAAC	AACACCCAA
FL/10/01 (GAAAAAAGGC	TGGGCAAAAC	AACACCCAA
NL/10/01 (GGAAAAAAGC	TGGGTAAAAC	AACACCCAA
NL/2/02 (A)	GAAAAAAGC	TGGGCAAAAC	AACACCCAA
NL/17/00 (GAAAAGAAAC	TGGGCAAAAC	AGCATCCAA
NL/1/81 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCACCFAA
NL/1/93 (A)	GAAAAGAAAC	TGGGCAAAAC	AACACTCAA
NL/2/93 (A)	GAAAAGAAAC	TGGGCAAAAC	AACACTCAA
NL/3/93 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCACCFAA
NL/1/95 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCACCFAA
NL/2/96 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCATCCAA
NL/3/96 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCACCFAA
NL/22/01 (GAAAAGAAAC	TGGGCAAAAC	AACACCAAA
NL/24/01 (GAAAAGAAAC	TGGGCAAAAC	AACACCAAA
NL/23/01 (GAAAAGAAAC	TGGGCAAAAC	AACACCCAA
NL/29/01 (GAAAAGAAAC	TGGGCAAAAC	AGCATCCAA
NL/3/02 (A)	GAAAAGAAAC	TGGGCAAAAC	AGCATCCAA
NL/1/99 (p)	GGAATAAGAA	GAGGCAAAA-	---ATTCAA
NL/11/00 (GGAATAAGAA	GAGGCAAAA-	---ATTCAA
NL/12/00 (GGAATAAGAA	GAGGCAAAA-	---ATTCAA
NL/5/01 (B)	GGAATAAGAA	GAGGCAAAA-	---ATTCAA
NL/9/01 (B)	GGAATAAGAA	GAGGCAAAA-	---ATTCAA
NL/21/01 (GGAATAAGAA	GAGGCAAGA-	---ATTCAA
NL/1/94 (p)	GAAATAAGAA	GAAGCTAAA-	---ATTCAA
NL/1/82 (B)	GAAATAAGAA	GAAGCTAAA-	---ATTCAA
NL/1/96 (B)	GAAATAAGAA	GAAGCTAAA-	---ATTCAA
NL/6/97 (B)	GAAATAAGAA	GAAGCTAAA-	---ATTCAA
NL/9/00 (B)	GAAATAAGAA	GAAGCTAAA-	---ATTCAA
NL/3/01 (B)	GAATTAAGAA	GAAGCTAAA-	---ATTCAA
NL/4/01 (B)	GAATTAAGAA	GAAGCTAAA-	---ATTCAA

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UK/5/01 (B . GAAATAAGAA GAAGCTAAA- ---ATTCAA

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Alignment: G Protein

	
		5	15	25	35	45	55
NL/1/00 (p	MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
BR/2/01 (A	MEVKVENIRT	IDMLKASVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
FL/4/01 (A	MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
FL/3/01 (A	MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
FL/8/01 (A	MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
FL/10/01 (MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/10/01 (MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/2/02 (A	MEVKVENIRT	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/17/00 (MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/1/81 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/1/93 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/2/93 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/3/93 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/1/95 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/2/96 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/3/96 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/22/01 (MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/24/01 (MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/23/01 (MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/29/01 (MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/3/02 (A	MEVKVENIRA	IDMLKARVKN	RVARSKCFKN	ASLVVIGITT	LSIALNIYLI	INYKMQKNTS	
NL/1/99 (p	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/11/00 (MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/12/00 (MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/5/01 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/9/01 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/21/01 (MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDHATLRNMI	
NL/1/94 (p	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/1/82 (B	MEVRVENIRT	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/1/96 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/6/97 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/9/00 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/3/01 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
NL/4/01 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
UK/5/01 (B	MEVRVENIRA	IDMFKAKIKN	RIRSSRCYRN	ATLILIGLTA	LSMALNIFLI	IDYATLKQMT	
	
		65	75	85	95	105	115
NL/1/00 (p	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
BR/2/01 (A	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
FL/4/01 (A	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
FL/3/01 (A	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
FL/8/01 (A	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
FL/10/01 (ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
NL/10/01 (ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
NL/2/02 (A	ESEHHTSSSP	MESSRETPTV	PTDNSDTNNS	PQHPTQQSTE	GSTLYFAASA	SSPETEPTST	
NL/17/00 (ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/1/81 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/1/93 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/2/93 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/3/93 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/1/95 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/2/96 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/3/96 (A	ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	
NL/22/01 (ESEHHTSSPP	TESNKEASTI	PIDNPDINPN	SQHPTQQSTE	SPTLNPAASV	SPSETEPAST	

FIGURE 20

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NL/24/01 (ESEHHTSSPP	TESNKESTI	PIDNPDINPN	SQHPTQQSAE	SLTLYPTSSV	SSSETEPAST
NL/23/01 (ESEHHTSSPP	TESNKESTI	PIDNPDINPN	SQHPTQQSTE	SLTLYPTSSV	SSSETEPAST
NL/29/01 (ESEHHTSSPP	TESNKEASTI	STDNPDINPN	SQHPTQQSTE	NPTLNPAASA	SPSETESAST
NL/3/02 (A	ESEHHTSSPP	TESNKEASTI	STDNPDINPN	SQHPTQQSTE	NPTLNPAASA	SPSETESAST
NL/1/99 (p	KTENCANMPS	AEPSKKTPTMT	STAGPNTKPN	PQATQWTE	NSTSPVATPE	GHPYTGTTQT
NL/11/00 (KTENCANMPS	AEPSKKTPTMT	STAGPSTEPN	PQATQWTE	NSTSPAATLE	SHPYTGTTQT
NL/12/00 (KTENCANMPP	AEPSKKTPTMT	STAGPNTKPN	PQATQWTE	NSTFPAATSE	GHLHTGTTQT
NL/5/01 (B	KTENCANMPP	AEPSRKTPTMT	STAGPNTKPN	PQATQWTE	NSTSPAATPE	GHLHTGTTQT
NL/9/01 (B	KTENCANMPP	AEPSKKTPTMT	STAGLNTKPN	PQATQWTE	NSTSPAATPE	GHLHTGTTQT
NL/21/01 (KTENCANMPP	AEPSKKTPTMT	STAGPNTKPN	PQATQWTE	NSTSPAATPE	GHLHTGTTQT
NL/1/94 (p	KVEHCVMMP	VEPSKKTPTMT	SAVDLNTKPN	PQATQLAAE	DSTSLAATSE	DHLHTGTTPT
NL/1/82 (B	KVEHCVMMP	VEPSKKTPTMT	STVDSSTGPN	PQATTQWTE	DSTSLAATSE	DHLHTGTTPT
NL/1/96 (B	KVEHCVMMP	VEPSKKTPTMT	SAVDLNTKLN	PQATQLTTE	DSTSLAATSE	DHLHTGTTPT
NL/6/97 (B	KVEHCVMMP	VEPSKKTPTMT	SAVDLNTKLN	PQATQLTTE	DSTSLAATSE	GHPHTGTTPT
NL/9/00 (B	KVEHCVMMP	VEPSKKTPTMT	SAVDSNTKPN	PQATQLTTE	DSTSLAATLE	DHPHTGTTPT
NL/3/01 (B	RVEHCVMMP	VEPSKKTPTMT	SAVDLNTKPN	PQATQLTTE	DSTSLAATLE	GHLHTGTTPT
NL/4/01 (B	RVEHCVMMP	VEPSKKTPTMT	SAVDLNTKPN	PQATQLTTE	DSTSPAATLE	GHLHTGTTPT
UK/5/01 (B	KVEHCVMMP	VEPSKKTPTMT	SAVDLNTKPN	PQATQLTTE	DSTSLAATLE	DHPHTGTTPT
.....						
	125	135	145	155	165	175
NL/1/00 (p	PDTTNRPPFV	DTHTTPPSAS	RTKTSPAVHT	KNNPRTSSR-	-----THSP	RATTRTARRT
BR/2/01 (A	PDTTNRPPFV	DTHTTPPSAS	RTKTSPAVHT	KNNPRTSSR-	-----THSP	RATTRTARRT
FL/4/01 (A	PDTTNRPPFV	DTHTTPPSAS	RTKTSPAVHT	KNNPRISSR-	-----THSP	WATTRTARRT
FL/3/01 (A	PDTTDRPPFV	DTHTTPPSAS	RTKTSPAVHT	KNNPRISSR-	-----THSP	WATTRTARRT
FL/8/01 (A	PDTTDRPPFV	DTHTTPPSAS	RTKTSPAVHT	KNNPRISSR-	-----THSP	WATTRTARRT
FL/10/01 (PDTTSRPPFV	DTHTTPPSAS	RTRTSPAVHT	KNNPRVSPR-	-----THSP	WAMTRTVRGT
NL/10/01 (PDTTSRPPFV	DTHTTPSSAS	RTKTSPAVHT	KNNLRISPR-	-----THSP	WAMTRTVRGT
NL/2/02 (A	PDTTSRPPFV	DTHTTPSSAS	RIRTSAPVHT	KNNLRISPR-	-----THSP	WAMTRTVRGT
NL/17/00 (PDTTNRLSSV	DRSTAQPSES	RTKTPTVHT	INNPNNTASS-	-----THSP	RTTTKAIRRA
NL/1/81 (A	PDTTNRLSSV	DRSTTQPSES	RTKTPTVHT	KNNPSTVSR-	-----TQSP	RATTKAVLRA
NL/1/93 (A	PDTTNRLSSA	DRSTTQPSES	RTKTKLTVHT	KNNLSTASS-	-----TQSP	RATTKAVLRD
NL/2/93 (A	PDTTNRLSSA	DRSTTQPSES	RTKTKLTVHT	KNNLSTASS-	-----TQSP	RATTKAVLRD
NL/3/93 (A	PDTTNRLSSV	DRSTTQPSES	RTKTKLTVHK	KNIPSTVSR-	-----TQSS	RATTKAVLRA
NL/1/95 (A	SDTTSRLSSV	DRSTTQPSES	RARTKPTVHK	KNIPSTVSR-	-----TQSP	RATTKAVLRA
NL/2/96 (A	PDTTNRLSSV	DRSTAQPSES	RTKTPTVHT	RNNPSTASS-	-----TQSP	RVTTKAILRA
NL/3/96 (A	SDTTSRLSSV	DRSTTQPSES	RARTKPTVHK	KNIPSTVSR-	-----TQSP	RATTKAVLRA
NL/22/01 (PGITNHLFSV	DRSTTQPSES	RTKTNRIVHK	KNISSTVSR-	-----TQSP	RTTAKAVPRA
NL/24/01 (PGITNHLFSV	DRSTTQPSES	RTKTNRIVHK	KNISSTVSR-	-----TQSP	RTTAKAVPRA
NL/23/01 (PGITNHLFSV	DRSTTQPSES	RTKTNRIVHK	KNISSTVSR-	-----TQSP	RTTAKAVPRA
NL/29/01 (PDTTNRLSSV	DRSTVQPSN	RTKTKLTVHT	RNNLSTASS-	-----TQSP	RATTKAIRRA
NL/3/02 (A	PDTTNRLSSV	DRSTVQPSN	RTKTKLTVHT	RNNLSTASS-	-----TQSP	RATTKAIRRA
NL/1/99 (p	SDTTAPQQT	DKHTALPKST	NEQITQTTE	KKTIRATTQK	REKGKENTNQ	TTSTAATQTT
NL/11/00 (PDITAPQQT	DKHTALPKST	NEQITQTTE	KKTTRATTQK	REKEKENTNQ	TTSTAATQTT
NL/12/00 (PDITAPQQT	DKHTALPKST	NEQITQTTE	KKTTRATTQK	REKGKENTNQ	TTSTAATQTT
NL/5/01 (B	PDITAPQQT	DKHTALPKST	NEQITQTTE	KKTTRATTQK	REKGKENTNQ	TTSTAATQTT
NL/9/01 (B	PDITAPQQT	DKHTALPKST	NEQITQTTE	KKTTRATTQK	REKGKENTNQ	TTSTAATQTT
NL/21/01 (PDITAPQQT	DKHTALPKST	NEQITQTTE	KKTTRATTQK	REKGKENTNQ	TTSTAATQTT
NL/1/94 (p	PDATVSQQT	DEYTTLLRST	NRQTTQTTE	KKPTGATTK-	-----KETTR	TTSTAATQTL
NL/1/82 (B	LDATVSQQT	DKHTPLRST	NGQTTQTTE	KKPTRAIK-	-----KETTR	TTSTAATQTL
NL/1/96 (B	PDATVSQQT	DEHTTLLRST	NRQTTQTTE	KKPTGATTK-	-----KETTR	TTSTAATQTL
NL/6/97 (B	PDATVSQQT	DEHTTLLRST	NRQTTQTTE	KKPTGATTK-	-----KETTR	TTSTAATQTL
NL/9/00 (B	PDATVSQQT	DEHTTLLRST	NRQTTQTTE	KKPTRATTK-	-----KETTR	TTSTAATQTL
NL/3/01 (B	PDVTVSQQT	DEHTTLLRST	NRQTTQTAE	KKPTRATTK-	-----KETTR	TTSTAATQTL
NL/4/01 (B	PDATVSQQT	DEHTTLLRST	NRQTTQTAE	KKPTRATTK-	-----KETTR	TTSTAATQTL
UK/5/01 (B	PDATVSQQT	DEHTTLLRST	NRQTTQTAE	KKPTRATTK-	-----KETTR	TTSTAATQTL
.....						
	185	195	205	215	225	235
NL/1/00 (p	TTLRTSSTRK	RPSTASVQPD	ISATTHKNEE	ASPASPQTS	STTRIQRKSV	EANTSTTYNQ
BR/2/01 (A	TTLRTSSTRK	RPSTASVQPD	ISATTHKNEE	ASPASPQTS	STTRIQRKSV	EANTSTTYNQ

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FL/4/01 (A	TTLRTSSTRK	RPSTASVQPD	ISATTHKNEE	ASPASPQTS	STTRTQRKSV	EANTSTTYNQ
FL/3/01 (A	TTLRTSSTRK	RPSTASVQPD	ISATTHKNEE	ASPASPQTS	STTRTQRKSV	EANTSTTYNQ
FL/8/01 (A	TTLRTSSTRK	RPSTASVQPD	ISATTHKNEE	ASPASPQTS	STTRTQRKSV	EANTSTTYNQ
FL/10/01 (TTLRTSSTRK	RLSTASVQPD	SSATTHKHEE	TSPVSPQTS	STARPQRKGM	EASTSTTYNQ
NL/10/01 (TTLRTSSIRK	RPSTASVQPD	SSATTHKHEE	ASPVSPQASA	STARPQRKGM	EASTSTTYNQ
NL/2/02 (A	TTLRTSSIRK	RPSTASVQPD	SSATTHKHEE	ASPVSPQASA	STARPQRKGM	EASTSTTYNQ
NL/17/00 (TTFRMSSTGK	RPTTTLVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNNIK
NL/1/81 (A	TAFRTSSTRK	RPTTTSVQSD	SSTTTQNHEE	TSSANPQASA	STMQSQ----	----HTNNIK
NL/1/93 (A	TAFHTSSTGK	RPTTTSVQSG	SSTTTQNHEE	TSSSNPQASA	STMQDQ----	----DTNNTK
NL/2/93 (A	TAFHTSSTGK	RPTTTSVQSG	SSTTTQNHEE	TSSSNPQASA	STMQDQ----	----DTNNTK
NL/3/93 (A	TAFRTSSTGE	RPTTTSVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIVK
NL/1/95 (A	TAFRTSSTGE	GPTTTSVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIVK
NL/2/96 (A	TVFRMSSTGK	RPATTLVQSD	SSTTTQNHEE	TGSANSQASA	STMQN-----	----HSMNIK
NL/3/96 (A	TAFRMSSTGE	GPTTTSVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIAR
NL/22/01 (TALRTSSTGE	RPTTTPVQPD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIAR
NL/24/01 (TALRTSSTGE	RPTTTPVQPD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIAR
NL/23/01 (TALRTSSTGE	RPTTTPVQPD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNIAR
NL/29/01 (TTLRMSSTGR	RPTTTLVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNNIK
NL/3/02 (A	TTLRMSSTGR	RPTTTLVQSD	SSTTTQNHEE	TGSANPQASA	STMQN-----	----HTNNIK
NL/1/99 (p	NTTNQIRNAS	ETITTSDRPR	TDTTTQSSEQ	TTRATDPSSP	PHHAR-----	----GAKLK-
NL/11/00 (NTTNQIRNAS	ETITTSDRPR	IDTTTQSSDQ	TTRATDPSSP	PHHAQS-----	----GAKPK-
NL/12/00 (NTTNQIRNAS	ETITTSDRPR	TDSTTQSSEQ	TTRATDPSSP	PHHAQG-----	----SAKPK-
NL/5/01 (B	NTTNQIRNAS	ETITTSDRPR	TDSTTQSSEQ	TTQATDPSSP	AHHAQG-----	----SAKPK-
NL/9/01 (B	NTTNQIRNAS	ETITTSDRPR	TDSTTQSSEQ	TTRATDPSSP	PHHAQG-----	----SAKPK-
NL/21/01 (NTTNQIRNAI	ETITTSDRPR	TDSTTQSSEQ	TTRATDPSSH	PHHAQG-----	----SAKPK-
NL/1/94 (p	NTTNQTSYVR	EATTTARSR	NSATTQSSDQ	TTQAADPSSQ	PHHTQK-----	----STTTY
NL/1/82 (B	NTTNQTRNGR	ETTTARSR	NDATTQSSEQ	TNQTDPSSQ	PHHAIS-----	----TITITQ
NL/1/96 (B	NTTNQTSNGR	EATTTSTRSR	NGATTQNSDQ	TT-TADPSSQ	PHHTQK-----	----STTTY
NL/6/97 (B	NTTNQTSNGR	EATTTARSR	NGATTQNSDQ	ITQAADSSSQ	PHHTQK-----	----STTAY
NL/9/00 (B	NTTNQTSNGR	EATTTARSR	NNATTQSSDQ	TTQAAEPSSQ	SQHTQK-----	----STTTY
NL/3/01 (B	NTTNQTNNGR	EATTTARSR	NNATTQSSDQ	TTQAAEPSSQ	SQHTQK-----	----STTTY
NL/4/01 (B	NTTNQTSNGR	EATTTARSR	NNATTQSSDQ	TTQAAEPSSQ	SQHTKK-----	----STTTY
UK/5/01 (B	NTTNQTSNGR	EATTTARSR	NNATTQSSDQ	TTQAAEPNSQ	SQHTQK-----	----STTTY

....|....
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NL/1/00 (p	TS-----
BR/2/01 (A	TS-----
FL/4/01 (A	TS-----
FL/3/01 (A	TS-----
FL/8/01 (A	TS-----
FL/10/01 (TS-----
NL/10/01 (TS-----
NL/2/02 (A	TS-----
NL/17/00 (PN-----
NL/1/81 (A	PN-----
NL/1/93 (A	QN-----
NL/2/93 (A	QN-----
NL/3/93 (A	PN-----
NL/1/95 (A	PN-----
NL/2/96 (A	PN-----
NL/3/96 (A	PN-----
NL/22/01 (PN-----
NL/24/01 (PN-----
NL/23/01 (PN-----
NL/29/01 (PN-----
NL/3/02 (A	PN-----
NL/1/99 (p	-----
NL/11/00 (-----
NL/12/00 (-----
NL/5/01 (B	-----

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NL/9/01 (B . -----
 NL/21/01 (-----
 NL/1/94 (p NTDTSPPSS
 NL/1/82 (B HRHIFSK--
 NL/1/96 (B NTDTSPPSS
 NL/6/97 (B NTDTSPPSS
 NL/9/00 (B NTDSSLSS
 NL/3/01 (B NTDTSPPSS
 NL/4/01 (B NTDTSPPSS
 UK/5/01 (B NTDSSLSS

Phylogenetic analysis of hMPV F sequences

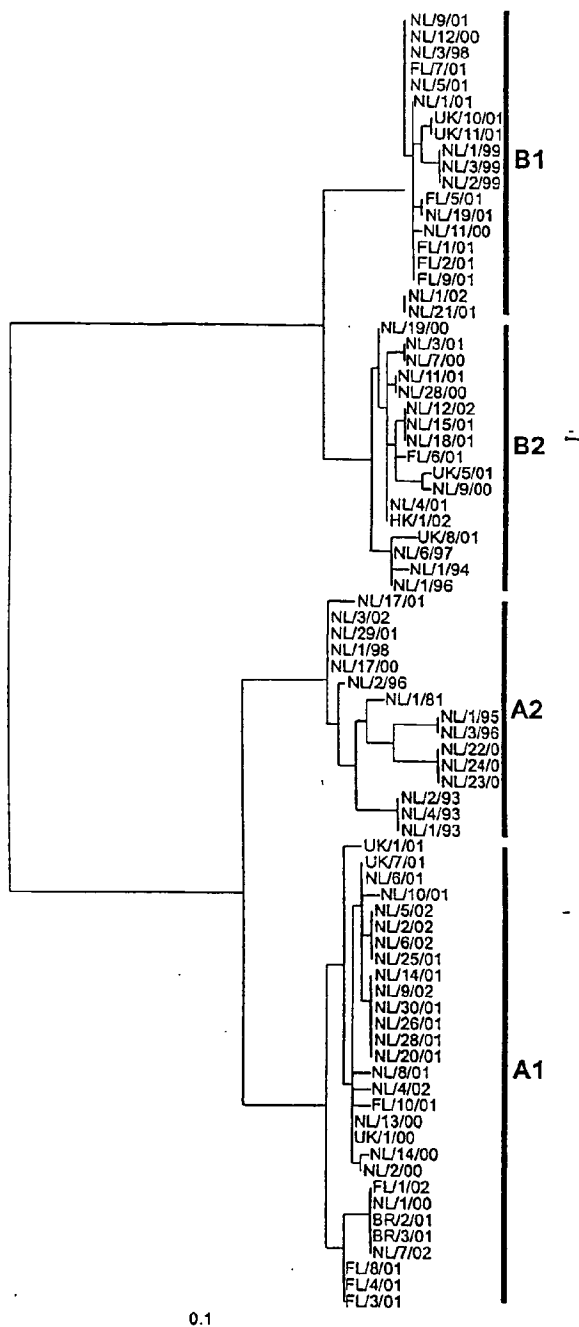


FIGURE 21

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Phylogenetic analysis of G sequences

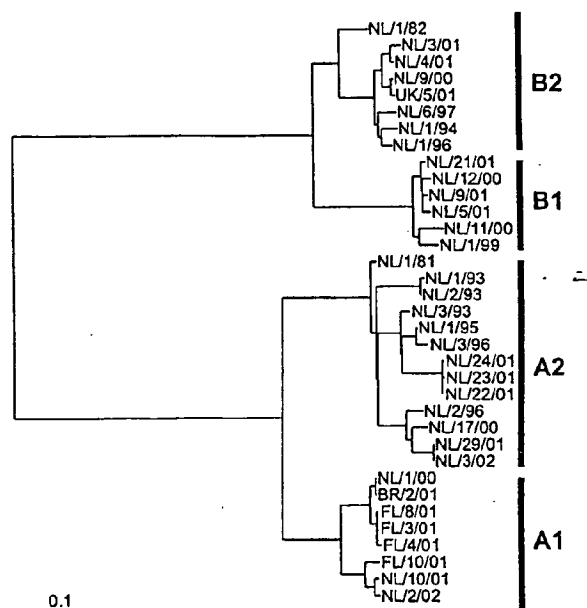


FIGURE 22

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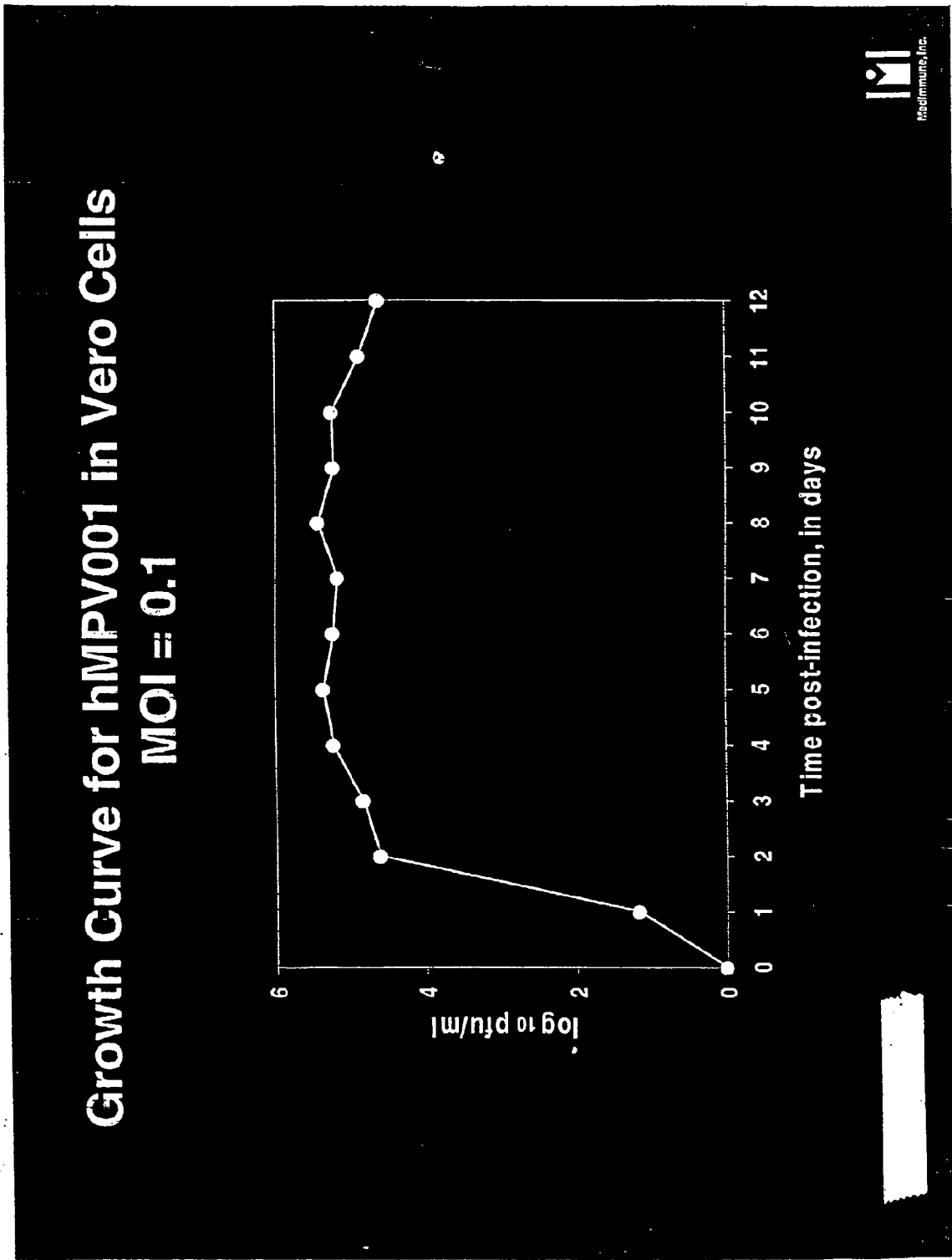


FIGURE 23

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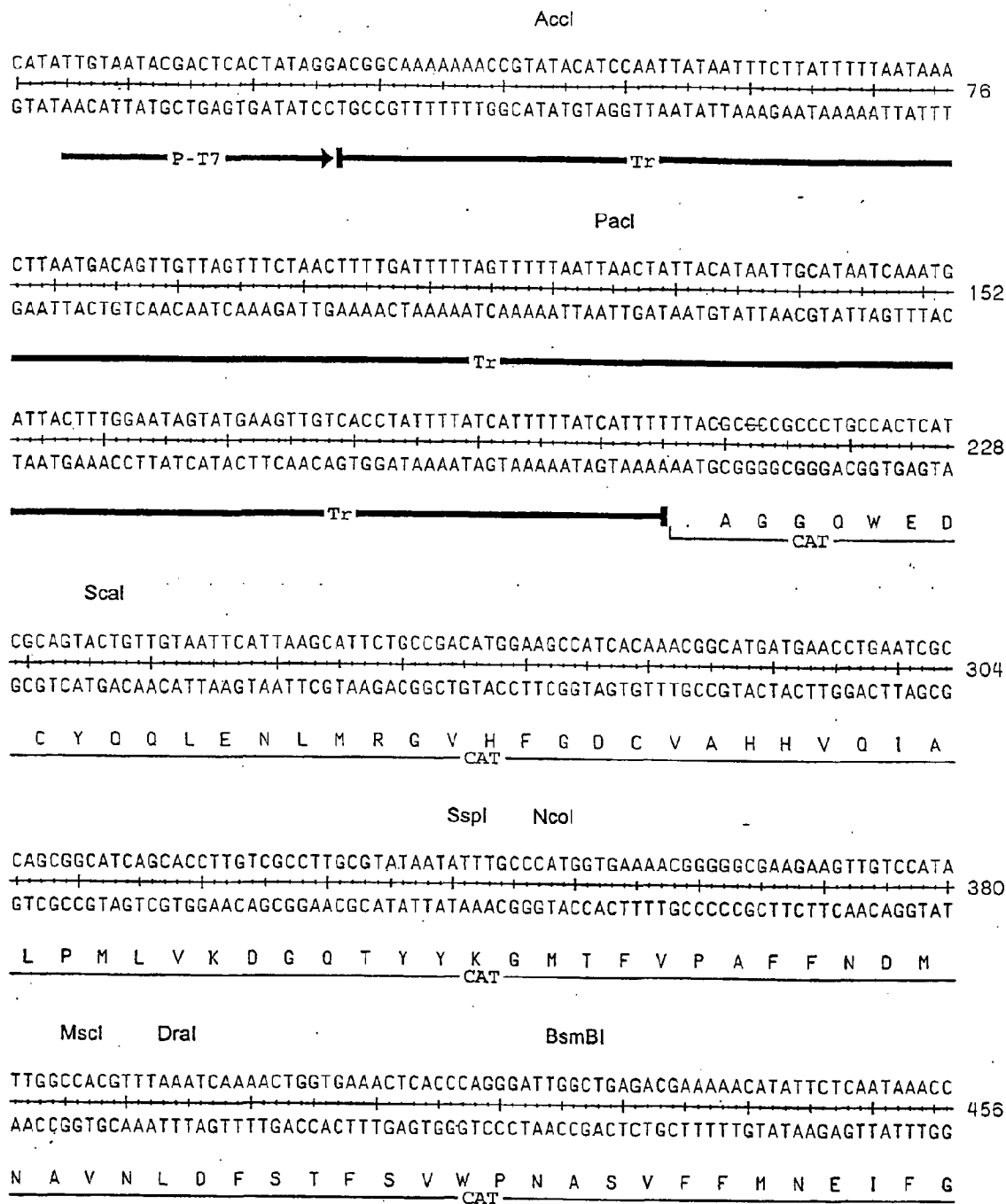


FIGURE 24

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CTTTAGGGAAATAGGCCAGGTTTTACCGTAACACGCCACATCTTGCGAATATATGTGTAGAACTGCCGGAAATC 532
GAAATCCCTTTATCCGGTCCAAAAGTGGCATTGTGCGGTGTAGAACGCTTATATACACATCTTTGACGGCCTTTAG

K P F Y A L N E G Y C A V D D S Y I H L F Q R F D
CAT

GTGCTGGTATTCAGTCCAGAGCGATGAAAACGTTTCAGTTTGCTCATGGAAAACGGTGTAAACAGGGTGAACACTA 608
CAGCACCATAAGTGAGGTCTCGCTACTTTTGCAAAGTCAAACGAGTACCTTTTGCCACATTGTTCCCACTTGTGAT

D H Y E S W L S S F T E T Q E H F V T Y C P H V S
CAT

EcoRI

TCCCATATCACCAGCTCACCGTCTTTTCATTGCCATACGGAATTCGGATGAGCATTATCAGCGGGGCAAGAATGT 684
AGGGTATAGTGGTCGAGTGGCAGAAAGTAACGGTATGCCCTTAAGGCCTACTCGTAAGTAGTCCGCCCGTTCTTACA

D W I V L E G D K M A M R F E P H A N M L R A L I H
CAT

DraI

PvuII

GAATAAAGGCCGGATAAACTTGTGCTTATTTTTCTTTACGGTCTTTAAAAAGGCCGTAATATCCAGCTGAACGGT 760
CTTATTTCCGGCCTATTTTGAACACGAATAAAAGAAATGCCAGAAATTTTCCGGCATTATAGGTCGACTTGCCA

I F A P Y F K H K N K K V T K L F A T I D L Q V T
CAT

CTGGTTATAGGTACATTGAGCAAGTGAATGCCTCAAAATGTTCTTTACGATGCGATTGGGATATATCAACG 836
GACCAATATCCATGTAACGTTCACTGACTTTACGGAGTTTACAAGAAATGCTACGCTAACCCCTATATAGTTGC

Q N Y T C Q A L S Q F A E F H E K R H S Q S I D V
CAT

AccI

AflIII
MluI

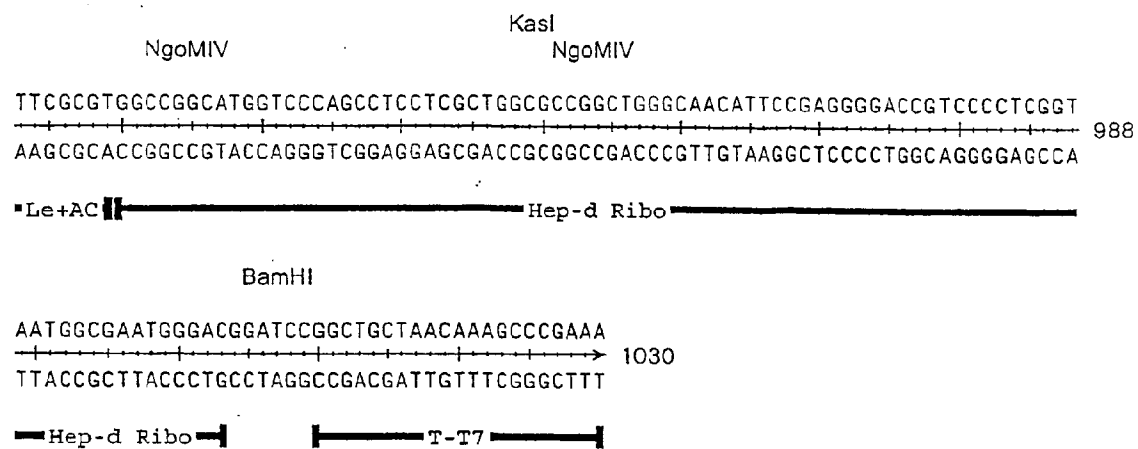
GNGGTATACCCAGTGATTTTTTCTCCATTTTCACTTGTCCCATATTTTTTGAATCTAATTTATACGCGTTTTT 912
CNCCATATGGGTCACTAAAAAAGAGGTAAAAGTGAACAGGGTATAAAAAACCTTAGATTAAATATGCGCAAAAA

? T Y G T I K K E M Le+AC
CAT

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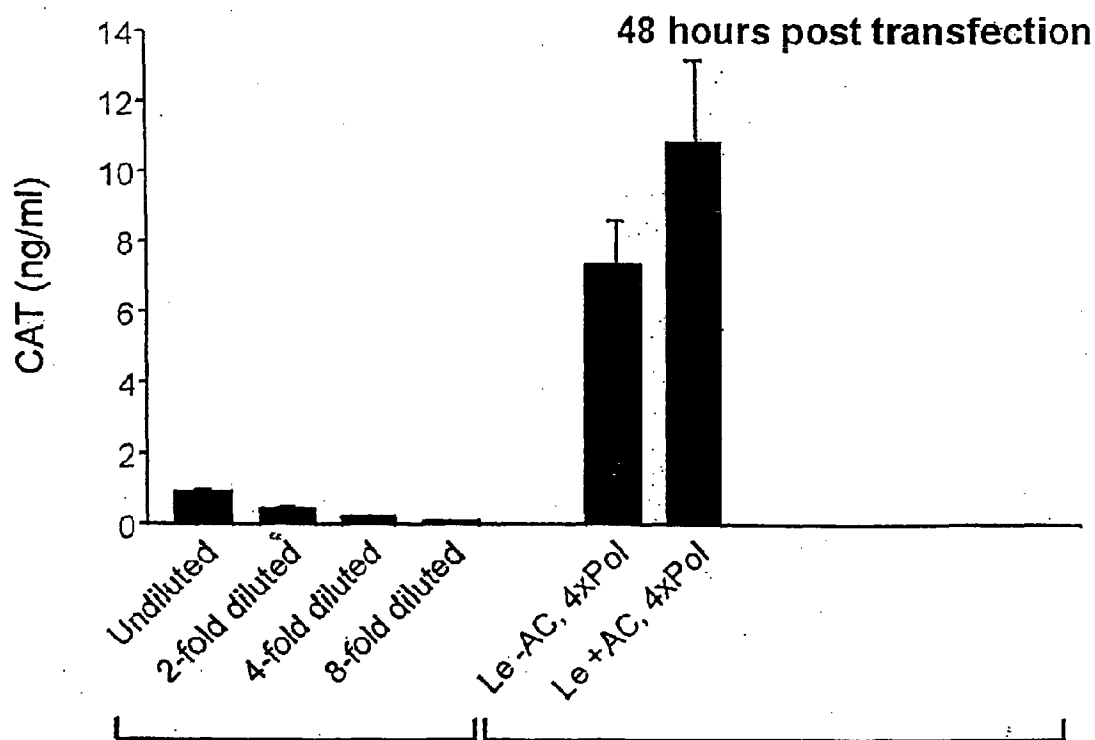
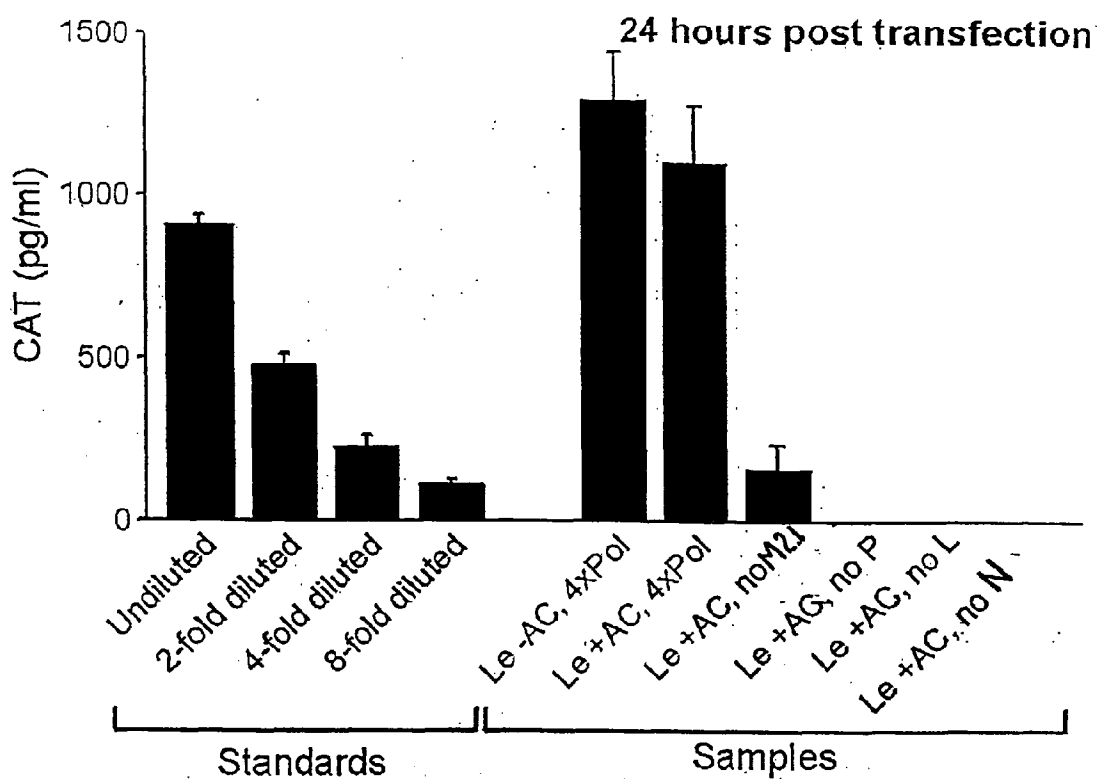


FIGURE 25

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Leader and Trailer Sequence Comparison

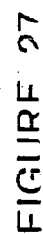
hMPV le	ACG CGA AAA AAA C GC GTA TA
hMPV tr	TGC CTT TTT G GC ATA T
APV le	ACG AGA AAA AAA C GC ATT CAA GCA GG
APV tr	TGC TCT TTT TTT G GC ATA AGT AGT TT
RSV A2 le	ACG GGA AAA AAT GCG TAC AAC AAA CTT
RSV A2 tr	TGC TCT TTT TTT CAC AGT TTT T
BRSV le	ACG CGA AAA AAT GCG TAT AAC AAA CCT GT
BRSV tr	TGC TCT TTT TTT CAT AGT TTT TG
HPIV3 le	ACC AAA CAA GAG AAG A GA CTT
HPIV3 tr	TGG TTT GTT CTC TTC T TG AGA
BPIV3 le	ACC AAA CAA GAG AAG A GA CTT
BPIV3 tr	TGG TTT GTT CTC TTT T TG AGA

Yellow color are non-complementary nucleotides between leader and trailer sequences

Green color is a nucleotide to be tested next: change C → A or G



FIGURE 2C



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Erasmus MC
Erasmus

hMPV full length clones

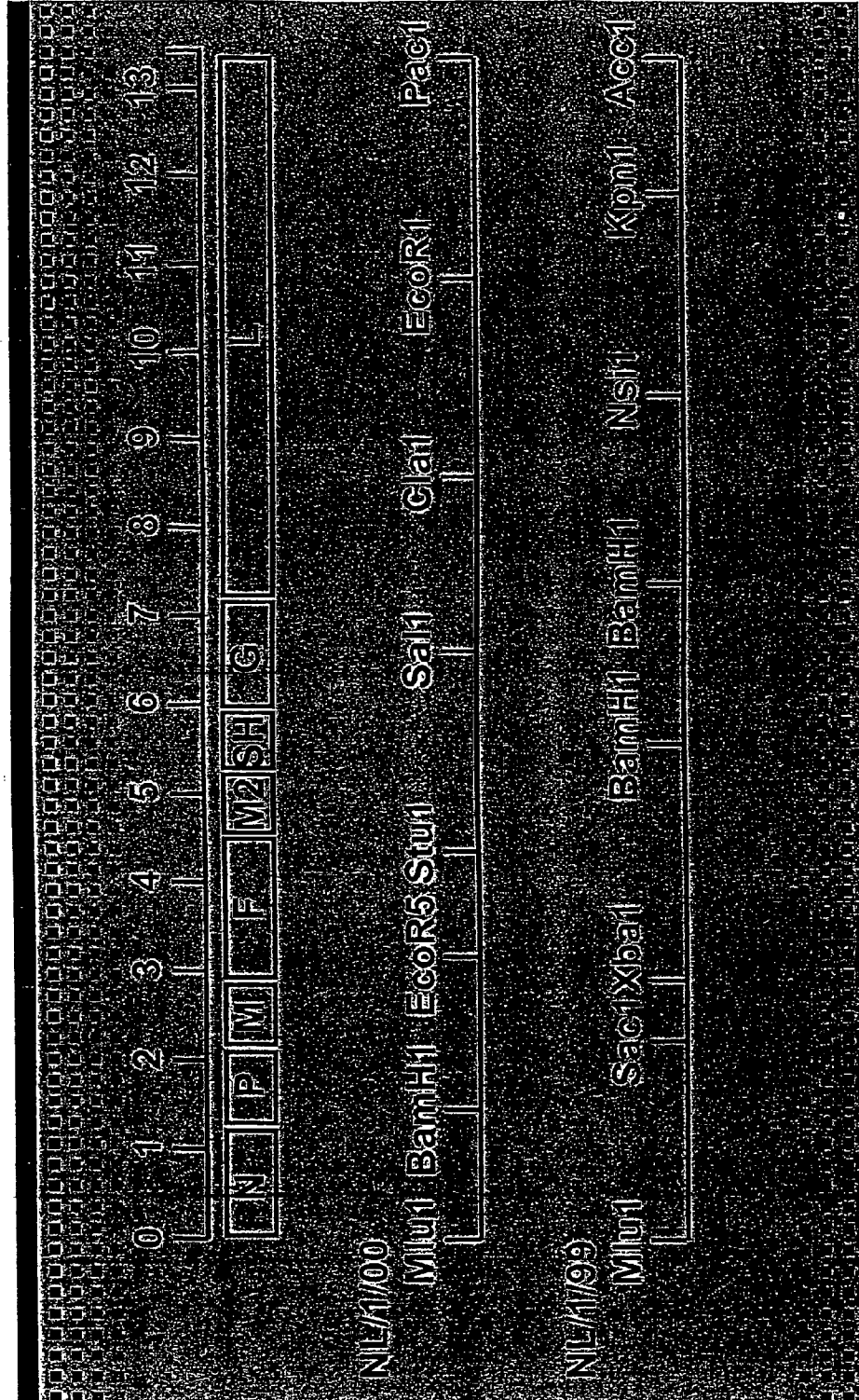


FIGURE 28

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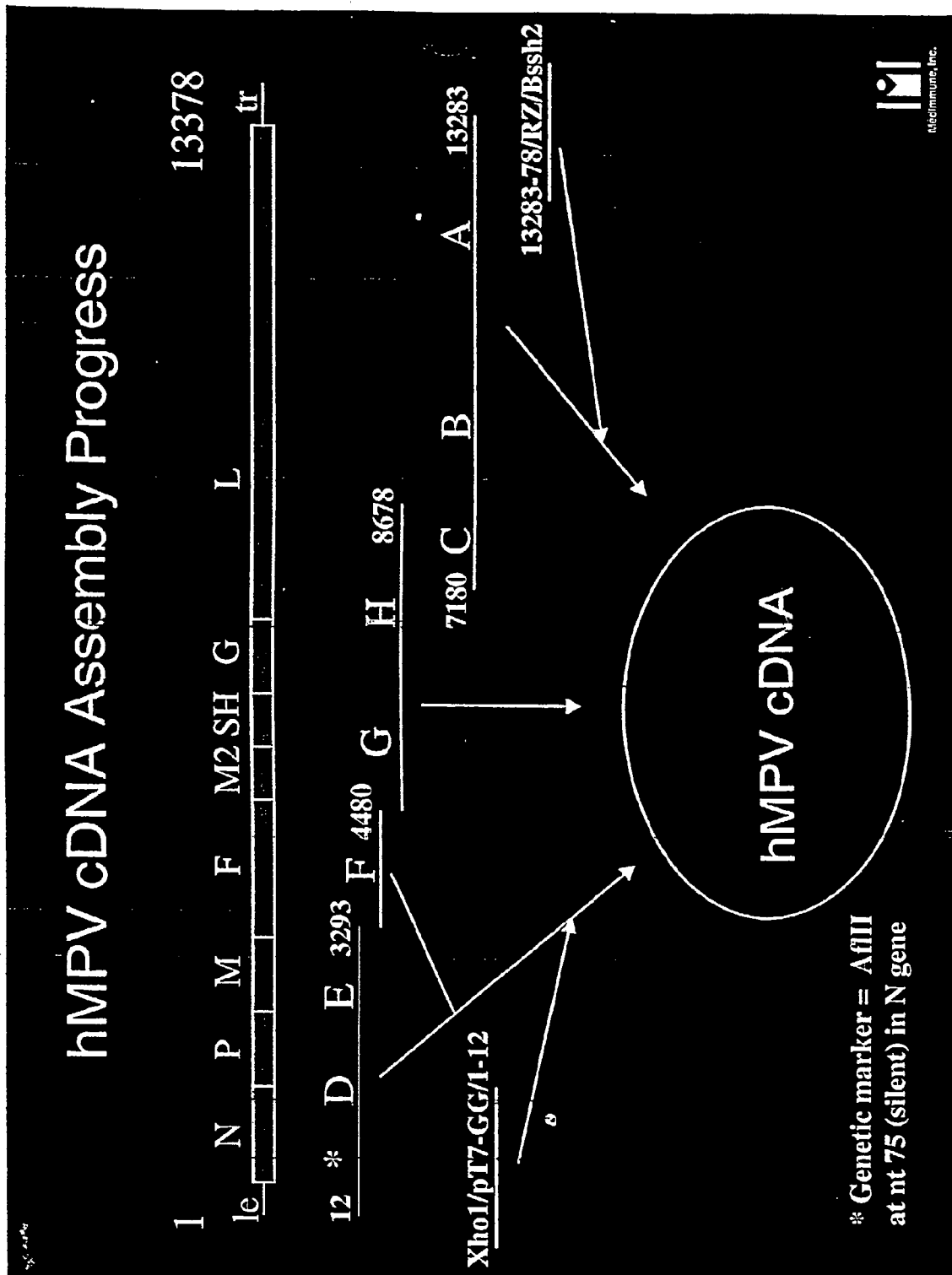


FIGURE 29A

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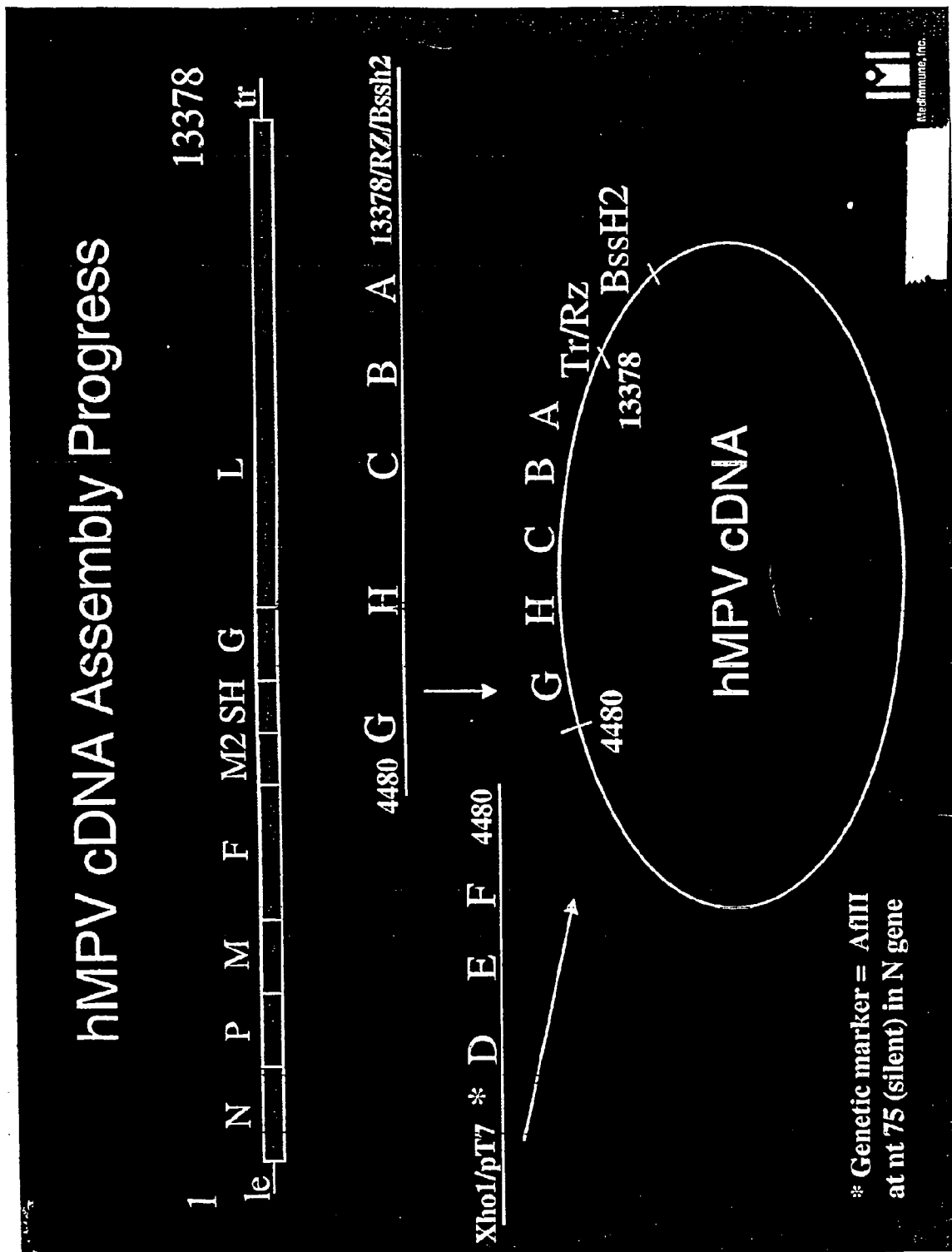
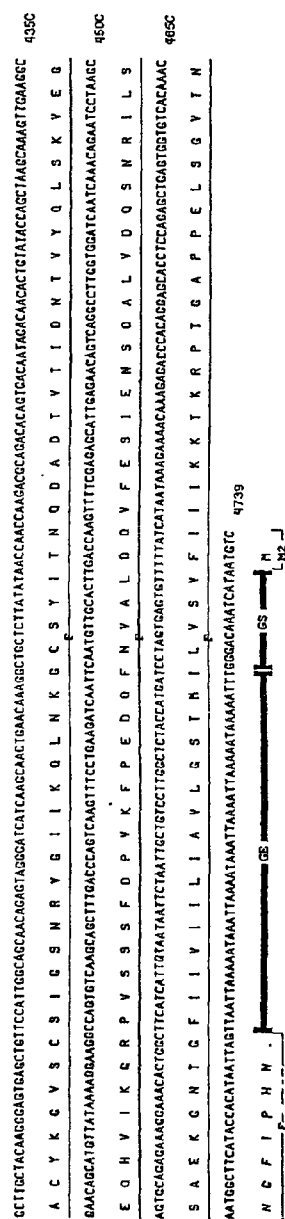


FIGURE 29B

FIGURE 30

FIGURE 30 · contd.

FIGURE 30 contd.



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CAGAGAAAACCTGTTCCACCTGTTAATGCTACTCTCCACCTCAATCTTAAGGAGCTGATTTCCCTTTAGTGAGACTAATGCAATTTGGTTCATGCTCTCTTAAGAGAGCTTACCTAAAGAAATGACAACACTGCAAAAGTTGCCATAGAG 15C
 DEKNCSYNYLPLPSYLYLKQVLSFSFSTNAISCLLKRPYLNKNDNTAKVAIE
 ATCCGTGTCGAGCATGTAGACTCAAAAATCCAGTCAATCTAAGATGCAAAATATACAGATTACAAGATAGAGGCCACTAAGCATGCAACATGAAATATGCAAGATCTACACAGTTGTGAGCTCACAATTATTAAACAGTTTTTA 30C
 NPVIEHVRLKNAVNSKHKISDYKIVEPVNMQH EIMKNVHSC E L T L L K Q F L
 ACAGGAGTAAAGAAATTTAGCACTCTCAAAATTAATATGATATGATGATTTGGCTCCAGTTAAGCTTACATCAGATGATACCTCAATCTTAAGTTTTATAGATGAGAAATTTATACCTAGCTGGGTAAAGCAATTCGTTTAGTAATTGGTAC 46C
 TRSKNISITLKLNMICDHLQ L K S T S D D T S I L S F I D V E F I P S V Y S N W F S N W Y
 AATCTCAAGAGTTCATCTGGAAATTCAGGAAAGAGCAAGTAATAGCACTGGTTCATCTGTGTGCTAGCTCATTCGGTAAATAGTTTGTGTATCATCATATCGATGTATAGTCAAGCAAGCAACAAAGCAAGCAAGTGTCTTC 60C
 NLNKLILEFRKEEVI RTGSI L C R S L G K L V F V S S Y G C I Y K S N K S K R V S F F
 ACATACAATCACTGTAACTGCAAGAGATGATCTTAAGTAGATTCAATGCAAAATTTTGTATATGGTACAGCAAGCTTGAATGAAATCAAGAGCGGTAGCGTGAAGAGTATTTGCAAGGCAATTTAAGCTTAAGCTATAT 75C
 TYNOLLTWKDVMLSRFFNANFCI W V S N S L N E N O E Q V C L R S N L O G I L T N K L Y
 SAAGCTGAGATTATGCTTATGTTATGTT 781
 ETVDYMLSLC

FIGURE 31 A

ATAGCTAGATAGATAACTTCTGATCAACATATCTCAGTCCAGACAAATAGATATGTTAACACTGSSDAAATGCTCATGCCACTATAAAGGTGCAAGAAACAGATCAGTTCTGACACAGAGAGAGATATTTTCCATGGCA 15C
 KLV D K I T S D Q H I F S P D K J D H L T L G K M L H P T I K G Q K T D Q F L N K R E N Y F H G
 ATAACTTATGAGCTTGTGTCAGAGCGTTAGCATGCTCATGCTGGGATATACAGAGCAATGTATAGAAATTAATATTTTTCAGAAACTGGGTGACCGGTTCATCCGATCATGCTTTTATGSACTTCAAAATATCTCAT 30C
 NWLIESSLALACHVCCJLT E Q C I E N N I F K K D W C D G F I S O H A F H O F K I F L
 GIGCTTTAAACTTAACCTTTTATETA 327
 CYFKTKLLC

FIGURE 31 B

+ = positive; - = negative; T = throatswabs; NO = nose swab; N = not done; ? = not sure; D = dead; 0 to 12: days post infection. 2^e infection is only tested on nose swabs.

nr	1 ^e infection	swab	0	1	2	3	4	5	8	10	11	12	2 ^e infection	0	1	2	3	4	5
1	00-1	T	-	+	+	+	-	+	+	+	-	-	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
2	00-1	T	-	+	+	+	+	+	-	-	-	D		N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	D		-	-	-	-	-	-
3	00-1	T	-	-	?	-	-	-	-	-	-	N	99-1	N	N	?	N	N	N
		NO	-	+	?	?	-	-	N	-	-	-		-	-	?	+	+	-
4	00-1	T	-	+	+	+	+	+	-	?	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	?	-	-		-	-	-	+	-	-
5	00-1	T	-	?	+	+	+	+	+	+	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
6	00-1	T	-	-	+	+	+	+	-	+	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	+	?		-	-	-	-	-	-
7	99-1	T	-	-	-	+	+	-	+	D	-	-		N	N	N	N	N	N
		NO	-	-	-	+	+	+	N	D	-	-		-	-	-	-	-	-
8	99-1	T	-	-	+	+	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	-	?	-	+	+	?	N	-	-	-		-	-	+	+	+	+
9	99-1	T	-	-	-	-	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	-	-	-	-	+	+	N	-	-	-		-	?	+	+	-	-
10	99-1	T	-	-	-	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	-		-	-	-	-	-	-
11	99-1	T	-	-	+	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	?	+	+	+	N	-	-	-		-	-	-	+	-	-
12	99-1	T	-	-	+	+	?	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	-		-	-	-	-	-	-

FIGURE 32

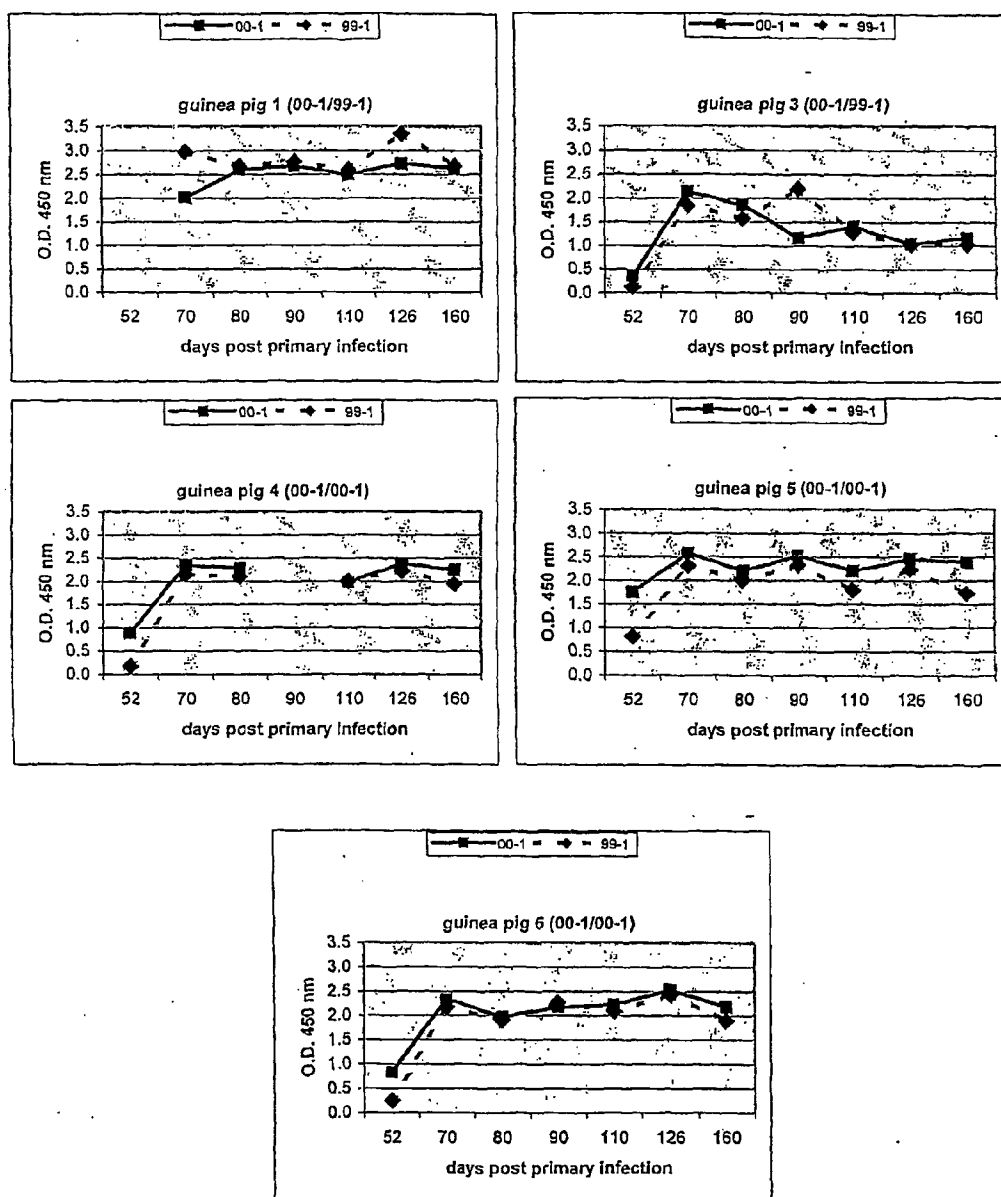


FIGURE 33A

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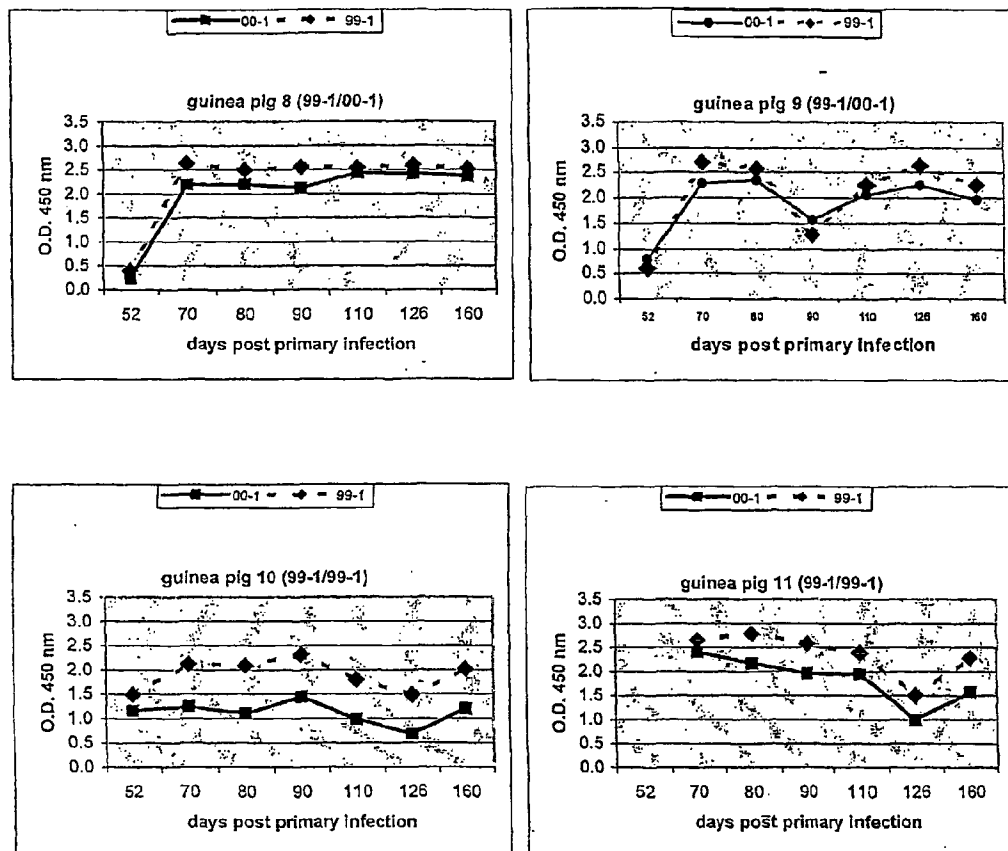


FIGURE 33B

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PCT/US03/05271

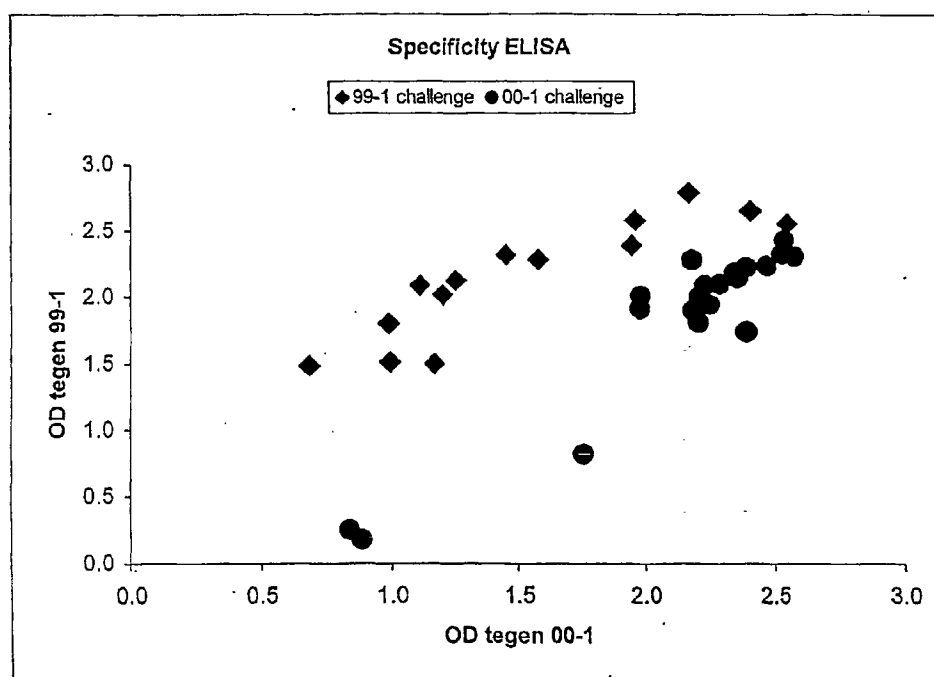


FIGURE 34

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PCT/US03/05271

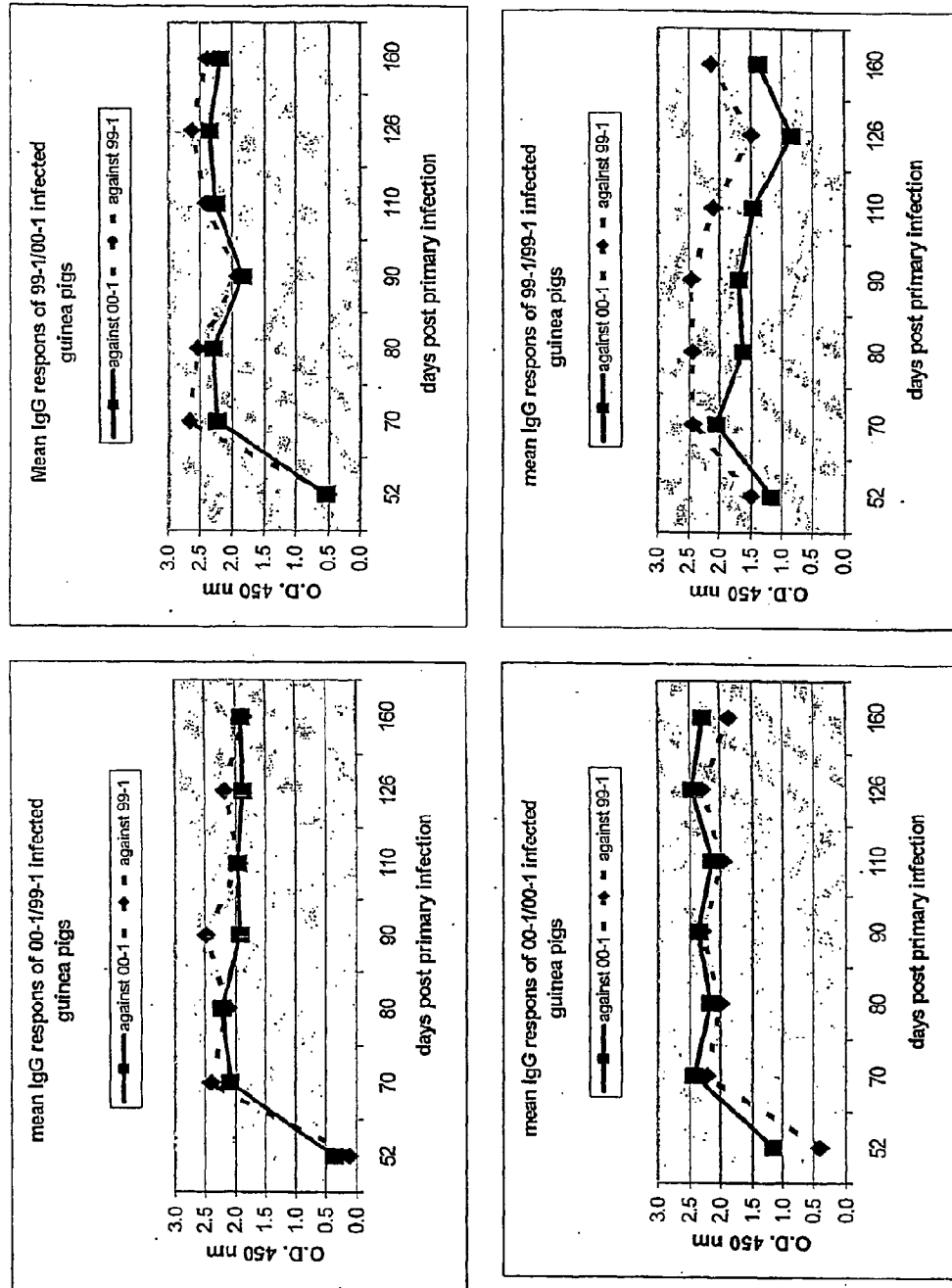


FIGURE 35

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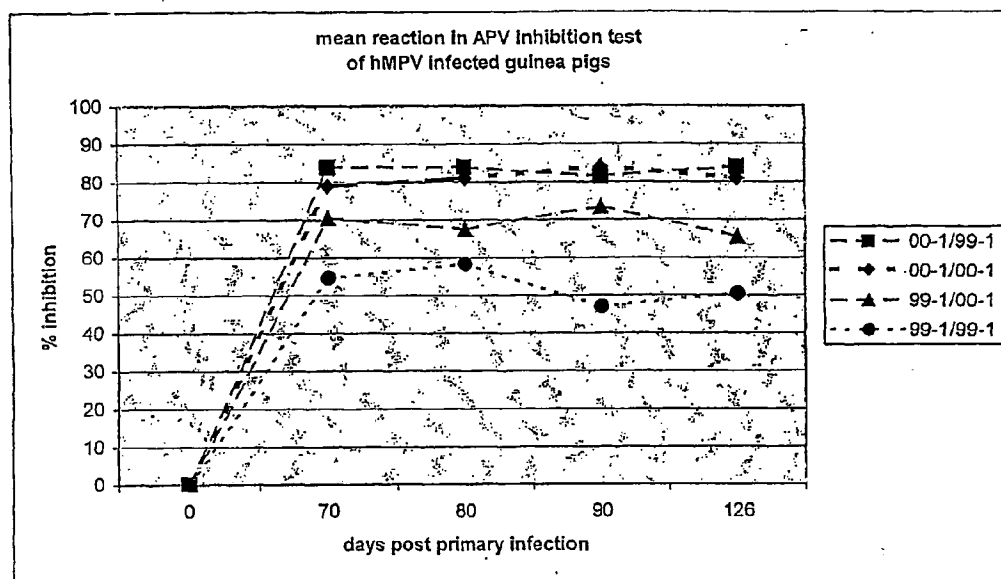


FIGURE 36

	Against 00-1	Against 99-1	Against APV-C
1 infection with 00-1	20-60	< 10	< 10
2 infections with 00-1	>320-1280	40-80	< 10-60
1 infection with 99-1	<10-60	10-80	< 10
2 infections with	20-40	80-400	<10-40

FIGURE 37

+ = positive; - = negative; N = not done; ? = not sure; 0 to 10: days post infection

nr	1 st infection	0	2	3	4	5	6	7	8	9	11	2 nd infect ion	0	1	2	3	4	5	7	10
3	00-1	-	-	-	+	+	+	+	+	N	-		-	+	+	+	+	-	?	-
6	00-1	-	+	+	+	+	+	+	-	-	-		-	+	+	+	+	+	-	-

FIGURE 38

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FIGURE 39A

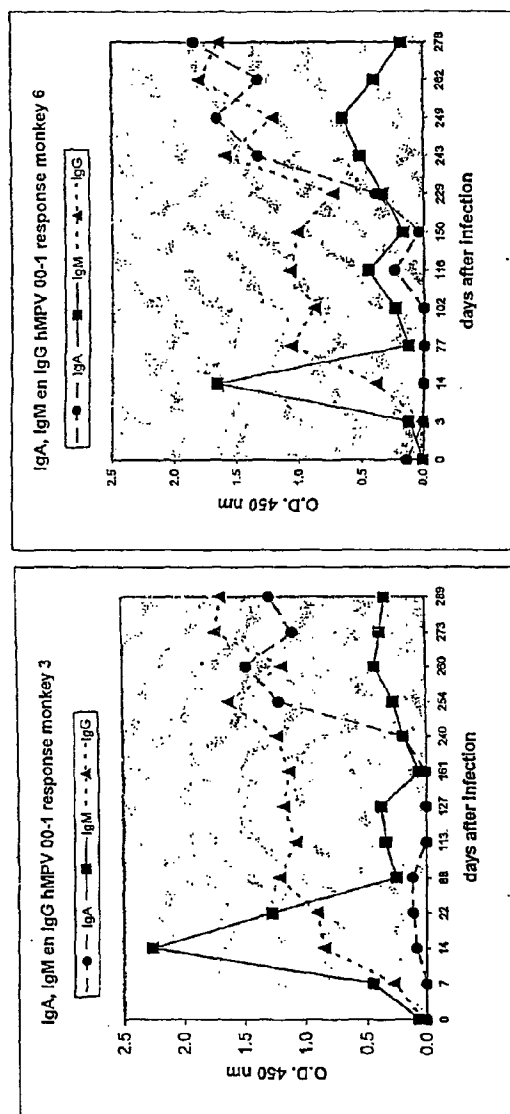
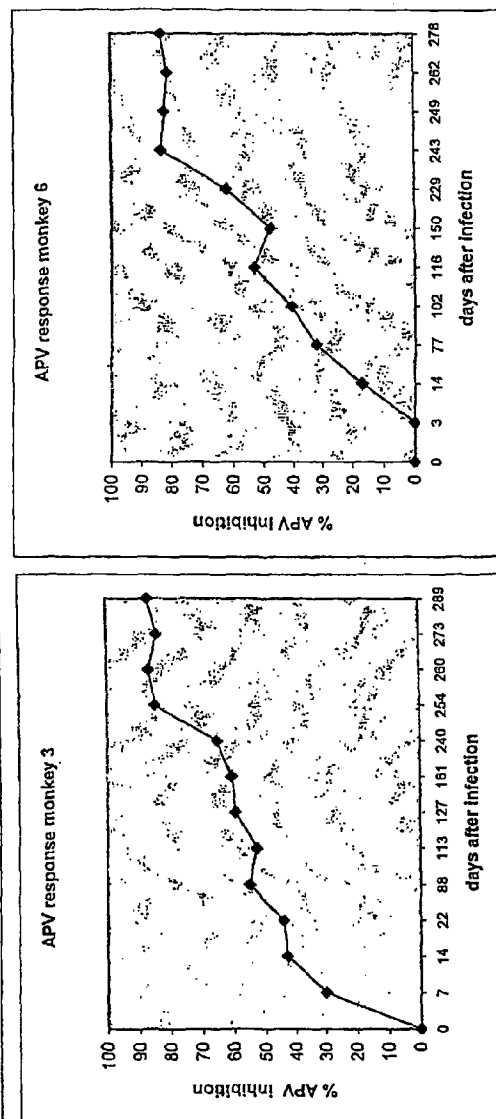


FIGURE 39B



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PCT/US03/05271

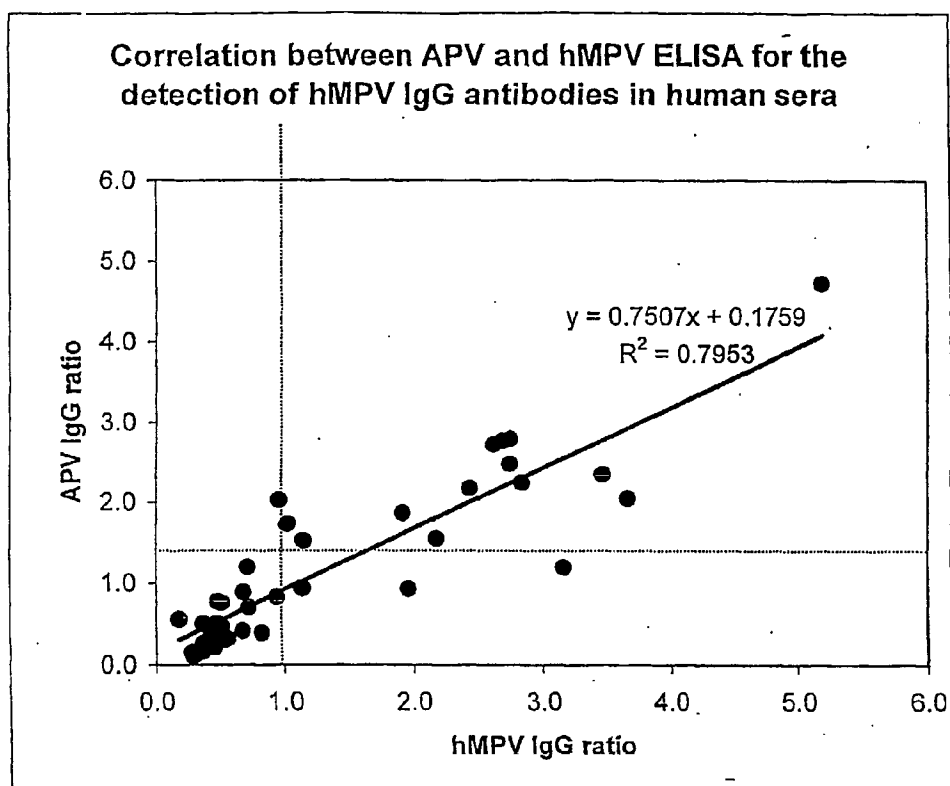


FIGURE 40

FIGURE 41

Comparison of two prototypic hMPV isolates with APV-A and APV-CDNA similarity matrices

<u>N</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,862	0,757	0,660
99-1	---	1,000	0,757	0,663
APVC	---	---	1,000	0,656
APVA	---	---	---	1,000

<u>P</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,811	0,677	0,588
99-1	---	1,000	0,674	0,593
APVC	---	---	1,000	0,584
APVA	---	---	---	1,000

<u>M</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,865	0,766	0,695
99-1	---	1,000	0,773	0,707
APVC	---	---	1,000	0,705
APVA	---	---	---	1,000

<u>F</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,838	0,706	0,662
99-1	---	1,000	0,716	0,655
APVC	---	---	1,000	0,685
APVA	---	---	---	1,000

<u>M2-1</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,863	0,764	0,668
99-1	---	1,000	0,744	0,657
APVC	---	---	1,000	0,670
APVA	---	---	---	1,000

<u>M2-2</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,861	0,648	0,486
99-1	---	1,000	0,675	0,486
APVC	---	---	1,000	0,463
APVA	---	---	---	1,000

<u>SH</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,688	N.A.	0,421
99-1	---	1,000	N.A.	0,380
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

<u>G</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,543	N.A.	0,262
99-1	---	1,000	N.A.	0,263
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

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<u>5'L</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,835	N.A.	0,596
99-1	---	1,000	N.A.	0,605
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 1500 nucleotides of 99-1 were available.
N.A.: sequence not available.

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Protein similarity matrices

<u>N</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,949	0,880	0,685
99-1	---	1,000	0,883	0,682
APVC	---	---	1,000	0,700
APVA	---	---	---	1,000
<u>P</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,860	0,683	0,552
99-1	---	1,000	0,676	0,549
APVC	---	---	1,000	0,528
APVA	---	---	---	1,000
<u>M</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,976	0,874	0,775
99-1	---	1,000	0,874	0,763
APVC	---	---	1,000	0,775
APVA	---	---	---	1,000
<u>F</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,938	0,810	0,677
99-1	---	1,000	0,803	0,674
APVC	---	---	1,000	0,719
APVA	---	---	---	1,000
<u>M2-1</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,946	0,844	0,719
99-1	---	1,000	0,834	0,703
APVC	---	---	1,000	0,704
APVA	---	---	---	1,000
<u>M2-2</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,901	0,563	0,246
99-1	---	1,000	0,577	0,232
APVC	---	---	1,000	0,191
APVA	---	---	---	1,000
<u>SH</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,570	N.A.	0,178
99-1	---	1,000	N.A.	0,162
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000
<u>G</u> 00-1	99-1	APVC	APVA	
00-1	1,000	0,326	N.A.	0,094
99-1	---	1,000	N.A.	0,107
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000
<u>5'L</u>	00-1	99-1	APVC	APVA
00-1	1,000	0,921	N.A.	0,600
99-1	---	1,000	N.A.	0,594
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 500 amino acid residues of 99-1 were available.

N.A.: sequence not available.

FIGURE 42A

Comparison of the coding sequences of 4 hMPV prototypes

N nt	NL/17/00	NL/1/99	NL/1/94	N aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.938	0.864	0.854	NL/1/00	0.994	0.954	0.961
NL/17/00		0.870	0.861	NL/17/00		0.956	0.964
NL/1/99			0.944	NL/1/99			0.984
P nt	NL/17/00	NL/1/99	NL/1/94	P aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.923	0.812	0.818	NL/1/00	0.955	0.863	0.867
NL/17/00		0.807	0.811	NL/17/00		0.857	0.863
NL/1/99			0.932	NL/1/99			0.959
M nt	NL/17/00	NL/1/99	NL/1/94	M aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.938	0.860	0.861	NL/1/00	0.988	0.976	0.976
NL/17/00		0.848	0.852	NL/17/00		0.972	0.972
NL/1/99			0.942	NL/1/99			1.000
F nt	NL/17/00	NL/1/99	NL/1/94	F aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.937	0.840	0.840	NL/1/00	0.979	0.940	0.946
NL/17/00		0.838	0.840	NL/17/00		0.942	0.949
NL/1/99			0.943	NL/1/99			0.987
M2 nt	NL/17/00	NL/1/99	NL/1/94	M2.1 aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.943	0.854	0.854	NL/1/00	0.983	0.946	0.951
NL/17/00		0.863	0.851	NL/17/00		0.951	0.957
NL/1/99			0.943	NL/1/99			0.978
M2.1 nt	NL/17/00	NL/1/99	NL/1/94	M2.2 aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.943	0.863	0.861	NL/1/00	0.957	0.901	0.915
NL/17/00		0.870	0.852	NL/17/00		0.887	0.901
NL/1/99			0.939	NL/1/99			0.985
M2.2 nt	NL/17/00	NL/1/99	NL/1/94	SH aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.953	0.861	0.865	NL/1/00	0.836	0.570	0.576
NL/17/00		0.870	0.875	NL/17/00		0.605	0.622
NL/1/99			0.967	NL/1/99			0.830
SH nt	NL/17/00	NL/1/99	NL/1/94	G aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.884	0.682	0.673	NL/1/00	0.652	0.309	0.341
NL/17/00		0.688	0.685	NL/17/00		0.337	0.338
NL/1/99			0.887	NL/1/99			0.651
G nt	NL/17/00	NL/1/99	NL/1/94	L aa	NL/17/00	NL/1/99	NL/1/94
NL/1/00	0.762	0.530	0.575	NL/1/00	0.986	0.942	0.938
NL/17/00		0.573	0.546	NL/17/00		0.944	0.939
NL/1/99			0.765	NL/1/99			0.985
L nt	NL/17/00	NL/1/99	NL/1/94				
NL/1/00	0.944	0.843	0.843				
NL/17/00		0.843	0.843				
NL/1/99			0.952				

FIGURE 42B

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Amino acid sequence alignment of two prototype hMPV isolatesNucleoprotein (N)

	10	20	30	40	50	60
00-1	MSLQGIHLS	DL SYKHAILKESQYTIKRDV	GGTTTAVTPSS	LQQEITLLC	GEILYAKH	ADYK 60
99-1	MSLQGIHLS	DL SYKHAILKESQYTIKRDV	GGTTTAVTPSS	LQQEITLLC	GEILYTKH	ADYK 60
	70	80	90	100	110	120
00-1	YAAEIGIQYI	STALGSE	RVQQILRNSGSEVQV	VLTRTYSLGK	IKNNKGED	LQMLDIHGVE 120
99-1	YAAEIGIQYI	CTALGSE	RVQQILRNSGSEVQV	VLTKTYSLGK	IKNSKGEEL	LQMLDIHGVE 120
	130	140	150	160	170	180
00-1	KSWVEEIDKEARKT	MTLLKES	SGNIPQNRPSAPDT	PIILLCVGALIFT	KLASTIEVGL	180
99-1	KSWIEEIDKEARKT	MTLLKES	SGNIPQNRPSAPDT	PIILLCVGALIFT	KLASTIEVGL	180
	190	200	210	220	230	240
00-1	ETTVRRANRVLS	DALKRYP	RM DIPKIARSFYDL	FEQKVYHRS	LFIEYGKALG	SSSTGSKA 240
99-1	ETTVRRANRVLS	DALKRYP	RI DIPKIARSFYEL	FEQKVYHRS	LFIEYGKALG	SSSTGSKA 240
	250	260	270	280	290	300
00-1	ESL FVNIFMQAYGAGQ	TMLRWGV	IARSSNNIMLGHVSVQ	AELKQVTEVYDL	VREMGPE	SG 300
99-1	ESL FVNIFMQAYGAGQ	TLLRWGV	IARSSNNIMLGHVSVQ	SELKQVTEVYDL	VREMGPE	SG 300
	310	320	330	340	350	360
00-1	LLHLRQSPKAGLL	SLANCPNFASV	VLGNASGLGI	IGMYRGRVPNTE	LFSAAESYAK	SLKE 360
99-1	LLHLRQSPKAGLL	SLANCPNFASV	VLGNASGLGI	IGMYRGRVPNTE	LFSAAESYAR	SLKE 360
	370	380	390			
00-1	SNKINFSSLGLTDEE	KEAAEHFLNVS	DDSQNDYE			394
99-1	SNKINFSSLGLTDEE	KEAAEHFLNMS	QDNQDDYE			394

FIGURE 43

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Phosphoprotein (P)

	10	20	30	40	50	60
00-1	MSFPEGKDILFMGNEAAKLAEAFQKSLRK	PGHKRSQSIIGKQNTVSETLELPTISRPAK	60			
99-1	MSFPEGKDILFMGNEAAKIAEAFQKSLKKS	SGHKRTQSIVGEKQNTVSETLELPTISKPAR	60			
	70	80	90	100	110	120
00-1	PTIPSEPKLAWTDKGGATKTEIKQAIKVM	PIEEEEESTKQVLPSSDGKTPAEKKLK	ST	120		
99-1	STILLKPKLAWADNSGITKITEKEATKTT	DPVEEEEFNEKKVLPSSDGKTPAEKKSK	ST	120		
	130	140	150	160	170	180
00-1	NTKKKVSFTFNEPGKYTKLEKDALD	LLSDNEEEDAESSILTFEERDTSSLSIEARLESIE	180			
99-1	SVKKKVSFTSNEPGKYTKLEKDALD	LLSDNEEEDAESSILTFEEKDTSSLSIEARLESIE	180			
	190	200	210	220	230	240
00-1	EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGVREELIADI	IKEAKGKAAEMMEEEMSQ	240			
99-1	EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGIREELIAEII	IKEAKGKAAEMMEEEMNQ	240			
	250	260	270	280	290	
00-1	RSKIGNGSVKLTEKAKELNKIVEDESTSGE	SEEEEEEPKDTQDNSQ	EDDIYQLIM	294		
99-1	RSKIGNGSVKLTEKAKELNKIVEDESTSGE	SEEEEEEPKETQDNNQ	EDDIYQLIM	294		

FIGURE 44

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Matrix protein (M)

	10	20	30	40	50	60	
						
00-1	MESYLVDITYQGIPYTAAVQVDLIEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL						60
99-1	MESYLVDITYQGIPYTAAVQVDLVEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL						60
	70	80	90	100	110	120	
						
00-1	YAASQNGPILKVNASQAQGAAMSVLPKKFEVNATVALDEYSKLEFDKLTVCVKTVYLTMT						120
99-1	YAASQNGPILKVNASQAQGAAMSVLPKKFEVNATVALDEYSKLEFDKLTVCVKTVYLTMT						120
	130	140	150	160	170	180	
						
00-1	KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNIPVTIPAFIKSVSIKESSESATVEAA						180
99-1	KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNIPVTIPAFIKSVSIKESSESATVEAA						180
	190	200	210	220	230	240	
						
00-1	ISSEADQALTQAKIAPYAGLIMMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISKICK						240
99-1	ISSEADQALTQAKIAPYAGLIMMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISRICK						240
	250						
						
00-1	TWSHQGTRYVLKSR						254
99-1	SWSHQGTRYVLKSR						254

FIGURE 45

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Fusion protein (F)

```

      10      20      30      40      50      60
00-1 MSWKVVIIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC 60
99-1 MSWKVMIIISLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC 60

      70      80      90     100     110     120
00-1 ADGPSLIKTELDLTKSALRELRTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA 120
99-1 TDGPSLIKTELDLTKSALRELRTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA 120

     130     140     150     160     170     180
00-1 GVAIAKTIRLESEVTAIKNALKKKTNEAVSTLGNGVRVLATAVRELKDFVSKNLTIRAINKN 180
99-1 GIAIAKTIRLESEVNAIKGALKQTNEAVSTLGNGVRVLATAVRELKEFVSKNLTISAINRN 180

     190     200     210     220     230     240
00-1 KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQ 240
99-1 KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSYMPTSAGQ 240

     250     260     270     280     290     300
00-1 IKLMLENRAMVRRKGFGLIGVYGSSVIYMVQLPIFGVIDTPCWIVKAAPSCSKKGNYA 300
99-1 IKLMLENRAMVRRKGFGLIGVYGSSVIYMVQLPIFGVIDTPCWIKAAPSCSEKKNYA 300

     310     320     330     340     350     360
00-1 CLLREDQGWYCNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYP 360
99-1 CLLREDQGWYCKNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSRECNINISTTNYP 360

     370     380     390     400     410     420
00-1 CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTI 420
99-1 CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNWVGIIKQLPKGCSYITNQDADTVTI 420

     430     440     450     460     470     480
00-1 DNTVYQLSKVEGEQHVIKGRPVSSSFDPVKFPEDQFNVALDQVFESIENSQALVDQSNRI 480
99-1 DNTVYQLSKVEGEQHVIKGRPVSSSFDPVKFPEDQFNVALDQVFESIENSQALVDQSNKI 480

     490     500     510     520     530
00-1 LSSAEKGNTGFIIVILVAVLGSTMIIVSVIIIIKKTKKPTGAPPELSGVTNNGGFIPHN 539
99-1 LNSAEKGNTGFIIVILVAVLGSTMISVSIIIIIKKTRKPTGAPPELNGVTNNGGFIPHS 539

```

FIGURE 46

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22K protein (M2-1)

	10	20	30	40	50	60	
						
00-1	MSRKAPCKYEV	RGKCNRGSECK	FNNHNYWSW	PDYLLIRSN	YLLNQLLRNT	DRADGLSIIS	60
99-1	MSRKAPCKYEV	RGKCNRGSDCK	FNNHNYWSW	PDYLLLRSN	YLLNQLLRNT	DKADGLSIIS	60
	70	80	90	100	110	120	
						
00-1	GAGREDRTQDF	VLGSTNVVQGY	IDNQGITKAA	ACYSLHNI	IKQLQEV	EVQRARDN	KLSD 120
99-1	GAGREDRTQDF	VLGSTNVVQGY	IDNQGITKAA	ACYSLHNI	IKQLQET	EVQRARDN	KLSD 120
	130	140	150	160	170	180	
						
00-1	SKHVALHNLV	LSYMEMSKTP	ASLINNLKRL	PREKLKKL	AKLIIDLS	SAGAE	NDSSYALQDS 180
99-1	SKHVALHNL	LILSYMEMSKTP	ASLINNLKRL	PREKLKKL	ARLIIDLS	SAGT	NDSSYALQDS 180
						
00-1	ESTNQVQ	187					
99-1	ESTNQVQ	187					

FIGURE 47

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M2-2 protein (M2-2)

		10	20	30	40	50	60
						
00-1	MTLHMPCKTVKALIKCSEHG	V	FITIE	V	DDMIWTHKDLKE	ALSDGIVKSHTNIY	NCYLEN 60
99-1	MTLHMPCKTVKALIKCSKHG	P	FITIE	A	DDMIWTHKELKE	ALSDGIVKSHTNIY	SCYLEN 60
		70					
						
00-1	IEIIYVK	AYLS	71				
99-1	IEIIYVK	AYLS	71				

FIGURE 48

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Short hydrophobic protein (SH)

		10	20	30	40	50	60																																																						
00-1	M	T	L	D	V	I	K	S	D	G	S	S	K	T	C	T	H	L	K	K	I	I	K	D	H	S	G	K	V	L	I	V	L	K	L	I	L	A	L	L	T	F	L	T	V	T	I	T	I	N	Y	I	K	V	E	N	N	L	Q	60	
99-1	M	K	T	L	D	V	I	K	S	D	G	S	S	E	T	C	N	L	K	K	I	I	K	K	H	S	G	K	V	L	I	A	L	K	L	I	L	A	L	L	T	F	F	T	A	T	T	V	N	Y	I	K	V	E	N	N	L	Q	60		
		70	80	90	100	110	120																																																						
00-1	I	C	Q	S	K	T	E	S	D	K	K	D	S	S	S	N	T	T	S	V	T	T	K	T	L	N	H	D	I	T	Q	Y	F	K	S	L	I	Q	R	Y	T	N	S	A	I	N	-	S	D	T	C	W	K	I	N	R	N	Q	119		
99-1	A	C	Q	P	K	N	E	S	D	K	K	V	T	K	P	N	T	T	S	T	I	R	P	T	P	D	P	T	V	V	H	L	K	R	L	I	Q	R	H	T	N	S	V	T	K	D	-	S	D	T	C	W	R	I	H	K	N	Q	120		
		130	140	150	160	170	180																																																						
00-1	T	N	I	T	T	Y	K	F	L	C	F	K	S	E	D	T	K	T	N	N	C	D	K	L	T	D	L	C	R	N	K	P	K	P	A	V	G	V	Y	H	I	V	E	C	H	C	I	Y	T	V	K	W	K	C	Y	H	Y	P	T	D	179
99-1	T	N	I	K	I	Y	K	F	L	C	S	G	F	T	N	S	K	G	T	D	C	E	E	P	T	A	L	C	D	K	K	L	K	T	I	V	E	K	H	R	K	A	E	C	H	C	L	H	T	T	E	W	G	C	L	H	P	---	177		
00-1	E	T	Q	S	183																																																							
99-1	-----					177																																																							

FIGURE 49

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Attachment glycoprotein (G)

	10	20	30	40	50	60	
00-1	MEVKVENIR	TIDMLKARVKNRVAR	SKCFKNASLV	LIGITL	LSIALNIYLI	INYKMKNTS	60
99-1	MEVRVENIR	AIDMFKAKIKNRIR	SSRCYRNATL	LILIGLTA	LSMALNIFLI	IDHATLRNMT	60
	70	80	90	100	110	120	
00-1	ESEHHTSSSP	MESSRETPTV	PTDMSDTNSS	POHPTQOSTE	GSTLYFAAS	ASSPETEPTST	120
99-1	KTENCANMPS	AEPSKKTPTMT	STAGPNTKPN	POQATQTTEN	STSPVATPE	GHPYTGTOT	120
	130	140	150	160	170	180	
00-1	PDITNRPPFV	DHTTPPSASR	TKTSFAVHTK	NNERTSSRTH	SPPRATTTR	TARRITTLRTS	180
99-1	SDITAPQOTT	DKHTAPLKST	NEQITOTTTE	KKTIRATTOK	REKGKENTN	QOTTSTAATOTT	180
	190	200	210	220	230		
00-1	STRKRPESTAS	VQPDISATTH	KNEEASPA	SPQTSASTTR	IQKSV	EANTSTTYNOTS	236
99-1	NTTNQIRNAS	ET-----IT	TSDRPRTD	TTTQSSEQT	TRATDPSS	PPPHA-----	224

FIGURE 50

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N-terminus of polymerase protein (L)

	10	20	30	40	50	60
00-1	MDP	LN	ESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRL	60		
99-1	MDP	FC	ESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVVEHVRL	60		
	70	80	90	100	110	120
00-1	KNA	VNS	SKMKISDYKIVEPVNMQHEIMKNVHSC	ELTLLKQFLTRSKNISTLKLNMICDWLQ	120	
99-1	RNA	VMT	KMKISDYKVVEPVNMQHEIMKNIHSC	ELTLLKQFLTRSKNISSLKLNMICDWLQ	120	
	130	140	150	160	170	180
00-1	LK	STSD	DT	SILSFIDVEFIP	SWVSNWFSNWN	LNKLILEFRKEEVIRTGSILCRSLGKLV
99-1	LK	STSD	NTSILNFIDVEFIP	VWVSNWFSNWN	LNKLILEFRREEVIRTGSILCRSLGKLV	180
	190	200	210	220	230	240
00-1	FV	VSSY	GCIVKSNKSKRV	SFFT	YNQLLTWKDVMLSRFNANFCI	WVSNLNLNENQEGGLGRLS
99-1	FV	VSSY	GCIVKSNKSKRV	SFFT	YNQLLTWKDVMLSRFNANFCI	WVSNLNLNENQEGGLGRLS
	250	260	270	280	290	300
00-1	NL	QGIL	TNKL	YETVDYMSLCCNEGFSLVKEFE	GFIMSEILRITEHAQFSTRFRNTLLNG	300
99-1	NL	QGM	LTNKL	YETVDYMSLCCNEGFSLVKEFE	GFIMSEILKITEHAQFSTRFRNTLLNG	300
	310	320	330	340	350	360
00-1	L	T	DQ	L	T	L
99-1	L	T	E	Q	L	S
	370	380	390	400	410	420
00-1	F	R	I	F	G	H
99-1	F	R	I	F	G	H
	430	440	450	460	470	480
00-1	L	K	V	L	S	K
99-1	L	K	V	L	S	K
	490					
00-1	K	R	L	I	W	S
99-1	K	K	L	I	W	S

FIGURE 51

A

[illegible]

hMPV Le: 3' UGCUCUUUUUUUGCGCAUUAUUAAUCUAAGGUUUUUUUUAUACCCU

hMPV Tr: 5' ACGAGAAAAAAC CGUAUACAUCCAAUUAUAAUUUCUUAUUUUU

hMEV Tr: 5' ACGAGAAAAAACCGUAACAUCCAAUUAUAUAUUCUUAUUUUA

APV Tr: 5' ACGAGAAAAAACCGAAUUCACAAAUUUUAGCUUUUAGUUUUU

hmpv Le: 3' UGCUCUUUUUUGCGCAUUUUAUCUAAGGUUUUUUAU-ACCC

APV 1e: 3' UGCUCUuuuuuuuGGGUA-AGUUCGUCCAGUUCUUUUUUUUUACCC

FIGURE 52

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1 10 90 30
00-1 1-9000 - - - - -	- - - - - G T A T A	A A T T A G A T T C
99-1 1-9000 A C G C G A A A A	A A C G C G T A T A	A A T T A A A T T C
. 40 50 60
00-1 1-9000 C A A A A A A T A	T G G G A C A A G T	G A A A A T G T C T
99-1 1-9000 C A A A C A A A - A	C G G G A C A A A T	A A A A A T G T C T
. 70 80 90
00-1 1-9000 C T T C A A G G G A	T T C A C C T G A G	T G A T T T A T C A
99-1 1-9000 C T T C A A G G G A	T T C A C C T A A G	T G A T C T A T C A
. 100 110 120
00-1 1-9000 T A C A A G C A T G	C T A T A T T A A A	A G A G T C T C A G
99-1 1-9000 T A T A A A C A T G	C T A T A T T A A A	A G A G T C T C A A
. 130 140 150
00-1 1-9000 T A C A C A A T A A	A A A G A G A T G T	G G G T A C A A C A
99-1 1-9000 T A C A C A A T A A	A A A G A G A T G T	A G G C A C C A C A
. 160 170 180
00-1 1-9000 A C T G C A G T G A	C A C C C T C A T C	A T T G C A A C A A
99-1 1-9000 A C T G C A G T G A	C A C C T T C A T C	A T T A C A A C A A
. 190 200 210
00-1 1-9000 G A A A T A A C A C	T G T T G T G T G G	A G A A A T T C T G
99-1 1-9000 G A A A T A A C A C	T T T T G T G T G G	G G A A A T A C T T
. 220 230 240
00-1 1-9000 T A T G C T A A A C	A T G C T G A C T A	C A A A T A T G C T
99-1 1-9000 T A C A C T A A A C	A C A C T G A T T A	C A A A T A T G C T
. 250 260 270
00-1 1-9000 G C A G A A A T A G	G A A T A C A A T A	T A T T A G C A C A
99-1 1-9000 G C T G A G A T A G	G A A T A C A A T A	T A T T T G C A C A
. 280 290 300
00-1 1-9000 G C T T T A G G A T	C A G A G A G A G T	G C A G C A G A T T
99-1 1-9000 G C T C T A G G A T	C A G A A A G A G T	A C A A C A G A T T
. 310 320 330
00-1 1-9000 C T G A G G A A C T	C A G G C A G T G A	A G T C C A A G T G
99-1 1-9000 T T G A G A A A C T	C A G G T A G T G A	A G T T C A G G T G
. 340 350 360
00-1 1-9000 G T C T T A A C C A	G A A C G T A C T C	T C T G G G G A A A
99-1 1-9000 G T T C T A A C C A	A A A C A T A C T C	C T T A G G G A A A
. 370 380 390
00-1 1-9000 A T T A A A A A C A	A T A A A G G A G A	A G A T T T A C A G
99-1 1-9000 G G C A A A A A C A	G T A A A G G G G A	A G A G C T G C A G

Figure 53

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00-1 1-9000	400 A T G T T A G A C A	420 T A C A C G G G G T	440 A G A G A A G A G C
99-1 1-9000	A T G T T A G A T A	T A C A T G G A G T	G G A A A A G A G T
00-1 1-9000	430 T G G G T A G A A G	440 A G A T A G A C A A	450 A G A A G C A A G G
99-1 1-9000	T G G A T A G A A G	A A A T A G A C A A	A G A G G C A A G A
00-1 1-9000	460 A A A A C A A T G G	470 C A A C C T T G C T	480 T A A G G A A T C A
99-1 1-9000	A A G A C A A T G G	T A A C T T T G C T	T A A G G A A T C A
00-1 1-9000	490 T C A G G T A A T A	500 T C C C A C A A A A	510 T C A G A G G C C C
99-1 1-9000	T C A G G T A A C A	T C C C A C A A A A	C C A G A G A C C T
00-1 1-9000	520 T C A G C A C C A G	530 A C A C A C C C A T	540 A A T C T T A T T A
99-1 1-9000	T C A G C A C C A G	A C A C A C C A A T	A A T T T T A T T A
00-1 1-9000	550 T G T G T A G G T G	560 C C T T A A T A T T	570 C A C T A A A C T A
99-1 1-9000	T G T G T A G G T G	C C C T A A T A T T	C A C T A A A C T A
00-1 1-9000	580 G C A T C A A C C A	590 T A G A A G T G G G	600 A C T A G A G A C C
99-1 1-9000	G C A T C A A C A A	T A G A A G T T G G	A T T A G A G A C T
00-1 1-9000	610 A C A G T C A G A A	620 G G G C T A A C C G	630 T G T A C T A A G T
99-1 1-9000	A C A G T T A G A A	G A G C T A A T A G	A G T G C T A A G T
00-1 1-9000	640 G A T G C A C T C A	650 A G A G A T A C C C	660 T A G A A T G G A C
99-1 1-9000	G A T G C A C T C A	A A A G A T A C C C	A A G G A T A G A T
00-1 1-9000	670 A T A C C A A A G A	680 T T G C C A G A T C	690 C T T C T A T G A C
99-1 1-9000	A T A C C A A A G A	T T G C T A G A T C	T T T T T A T G A A
00-1 1-9000	700 T T A T T T G A A C	710 A A A A A G T G T A	720 T C A C A G A A G T
99-1 1-9000	C T A T T T G A A C	A A A A A G T G T A	C T A C A G A A G T
00-1 1-9000	730 T T G T T C A T T G	740 A G T A T G G C A A	750 A G C A T T A G G C
99-1 1-9000	T T A T T C A T T G	A G T A C G G A A A	A G C T T T A G G C
00-1 1-9000	760 T C A T C A T C T A	770 C A G G C A G C A A	780 A G C A G A A A G T
99-1 1-9000	T C A T C T T C A A	C A G G A A G C A A	A G C A G A A A G T

Figure 53 cont'd

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00-1 1-9000	CTATTTGTTA	790	ATATATTTCAT	800	GCAAGCTTAT	810
99-1 1-9000	TTGTTTGTAA		ATATATTTTAT		GCAAGCTTAT	
00-1 1-9000	GGGGCCGGTC	820	AAACAATGCT	830	AAGGTGGGGG	840
99-1 1-9000	GGAGCTGGCC		AAACAATGCT		AAGGTGGGGT	
00-1 1-9000	GTCATTGCCA	850	GGTCATCCAA	860	CAATATAATG	870
99-1 1-9000	GTCATTGCCA		GATCATCCAA		CAACATAATG	
00-1 1-9000	TTAGGACATG	880	TATCCGTCCA	890	AGCTGAGTTA	900
99-1 1-9000	CTAGGGCATG		TATCTGTGCA		ATCTGAATTG	
00-1 1-9000	AAACAGGTCA	910	CAGAAGTCTA	920	TGACTTGGTG	930
99-1 1-9000	AAGCAAGTTA		CAGAGGTTTA		TGACTTGGTG	
00-1 1-9000	CGAGAAATGG	940	GCCCTGAATC	950	TGGACTTCTA	960
99-1 1-9000	AGAGAAATGG		GTCCTGAATC		TGGGCTTTTA	
00-1 1-9000	CATTTAAGGC	970	AAAGCCCAAA	980	AGCTGGACTG	990
99-1 1-9000	CATCTAAGAC		AAAGTCCAAA		GGCAGGGCTG	
00-1 1-9000	TTATCACTAG	1000	CCAACTGTCC	1010	CAACTTTGCA	1020
99-1 1-9000	TTATCATTTG		CCAATTGCCC		CAATTTTGTCT	
00-1 1-9000	AGTGTTGTTC	1030	TCGGAAATGC	1040	CTCAGGCTTA	1050
99-1 1-9000	AGTGTTGTTC		TTGGCAATGC		TTCAGGTCTA	
00-1 1-9000	GGCATAATCG	1060	GTATGTATCG	1070	AGGGAGAGTA	1080
99-1 1-9000	GGCATAATCG		GAATGTACAG		AGGGAGAGTA	
00-1 1-9000	CCAAACACAG	1090	AATTATTTTC	1100	AGCAGCTGAA	1110
99-1 1-9000	CCAAACACAG		AGCTATTTTC		TGCAGCAGAA	
00-1 1-9000	AGTTATGCCA	1120	AAAGTTTGAA	1130	AGAAAGCAAT	1140
99-1 1-9000	AGTTATGCCA		GAAGCTTAAA		AGAAAGCAAT	
00-1 1-9000	AAAATAAATT	1150	TCTCTTCATT	1160	AGGACTTACA	1170
99-1 1-9000	AAAATCAACT		TCTCTTCGTT		AGGGCTTACA	

Figure 53 cont'd

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		1180		1190		1200
00-1 1-9000	G A T G A A G A G A		A A G A G G C T G C		A G A A C A T T T C	
99-1 1-9000	G A T G A A G A A A		A A G A A G C T G C		A G A A C A C T T C	
		1210		1220		1230
00-1 1-9000	T T A A A T G T G A		G T G A C G A C A G		T C A A A A T G A T	
99-1 1-9000	T T A A A C A T G A		G T G G T G A C A A		T C A A G A T G A T	
		1240		1250		1260
00-1 1-9000	T A T G A G T A A T		T A A A A A A G T G		G G A C A A G T C A	
99-1 1-9000	T A T G A G T A A T		T A A A A A A C T G		G G A C A A G T C A	
		1270		1280		1290
00-1 1-9000	A A A T G T C A T T		C C C T G A A G G A		A A A G A T A T T C	
99-1 1-9000	A A A T G T C A T T		C C C T G A A G G A		A A G G A T A T T C	
		1300		1310		1320
00-1 1-9000	T T T T C A T G G G		T A A T G A A G C A		G C A A A A T T A G	
99-1 1-9000	T G T T C A T G G G		T A A T G A A G C A		G C A A A A A T A G	
		1330		1340		1350
00-1 1-9000	C A G A A G C T T T		C C A G A A A T C A		T T A A G A A A A C	
99-1 1-9000	C C G A A G C T T T		C C A G A A A T C A		C T G A A A A A A T	
		1360		1370		1380
00-1 1-9000	C A G G T C A T A A		A A G A T C T C A A		T C T A T T A T A G	
99-1 1-9000	C A G G T C A C A A		G A G A A C T C A A		T C T A T T G T A G	
		1390		1400		1410
00-1 1-9000	G A G A A A A A G T		G A A T A C T G T A		T C A G A A A C A T	
99-1 1-9000	G G G A A A A A G T		T A A C A C T A T A		T C A G A A A C T C	
		1420		1430		1440
00-1 1-9000	T G G A A T T A C C		T A C T A T C A G T		A G A C C T G C A A	
99-1 1-9000	T A G A A C T A C C		T A C C A T C A G C		A A A C C T G C A C	
		1450		1460		1470
00-1 1-9000	A A C C A A C C A T		A C C G T C A G A A		C C A A A G T T A G	
99-1 1-9000	G A T C A T C T A C		A C T G C T G G A A		C C A A A A T T G G	
		1480		1490		1500
00-1 1-9000	C A T G G A C A G A		T A A A G G T G G G		G C A A C C A A A A	
99-1 1-9000	C A T G G G C A G A		C A A C A G C G G A		A T C A C C A A A A	
		1510		1520		1530
00-1 1-9000	C T G A A A T A A A		G C A A G C A A T C		A A A G T C A T G G	
99-1 1-9000	T C A C A G A A A A		A C C A G C A A C C		A A A A C A A C A G	
		1540		1550		1560
00-1 1-9000	A T C C C A T T G A		A G A A G A A G A G		T C T A C C G A G A	
99-1 1-9000	A T C C T G T T G A		A G A A G A G G A A		T T C A A T G A A A	

Figure 53 cont'd

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	1570	1580	1590
00-1 1-9000	A G A A G G T G C T	A C C C T C C A G T	G A T G G G A A A A
99-1 1-9000	A G A A A G T G T T	A C C T T C C A G T	G A T G G G A A G A
	1600	1610	1620
00-1 1-9000	C C C C T G C A G A	A A A G A A A C T G	A A A C C A T C A A
99-1 1-9000	C T C C T G C A G A	G A A A A A A T C A	A A G T T T T C A A
	1630	1640	1650
00-1 1-9000	C T A A C A C C A A	A A A G A A G G T T	T C A T T T T A C A C
99-1 1-9000	C C A G T G T A A A	A A A G A A A G T T	T C C T T T A C A T
	1660	1670	1680
00-1 1-9000	C A A A T G A A C C	A G G G A A A T A T	A C A A A G T T G G
99-1 1-9000	C A A A T G A A C C	A G G G A A A T A C	A C C A A A C T A G
	1690	1700	1710
00-1 1-9000	A A A A A G A T G C	T C T A G A T T T G	C T C T C A G A T A
99-1 1-9000	A G A A A G A T G C	C C T A G A T T T G	C T C T C A G A C A
	1720	1730	1740
00-1 1-9000	A T G A A G A A G A	A G A T G C A G A A	T C T T C A A T C T
99-1 1-9000	A T G A G G A A G A	A G A C G C A G A A	T C C T C A A T C C
	1750	1760	1770
00-1 1-9000	T A A C C T T T T G A	A G A A A G A G A T	A C T T C A T C A T
99-1 1-9000	T A A C T T T T T G A	G G A G A A A G A T	A C A T C A T C A C
	1780	1790	1800
00-1 1-9000	T A A G C A T T T G A	G G C C A G A T T G	G A A T C A A T A G
99-1 1-9000	T A A G C A T T T G A	A G C T A G A C T A	G A A T C T A T A G
	1810	1820	1830
00-1 1-9000	A G G A G A A A T T	A A G C A T G A T A	T T A G G G C T A T
99-1 1-9000	A A G A G A A G T T	G A G C A T G A T A	T T A G G A C T G C
	1840	1850	1860
00-1 1-9000	T A A G A A C A C T	C A A C A T T G C T	A C A G C A G G A C
99-1 1-9000	T T C G T A C A C T	T A A C A T T G C A	A C A G C A G G A C
	1870	1880	1890
00-1 1-9000	C C A C A G C A G C	A A G A G A T G G G	A T C A G A G A T G
99-1 1-9000	C A A C A G C T G C	A C G A G A T G G A	A T T A G G G A T G
	1900	1910	1920
00-1 1-9000	C A A T G A T T G G	C G T A A G A G A G	G A A T T A A T A G
99-1 1-9000	C A A T G A T T G G	T A T A A G A G A A	G A G C T A A T A G
	1930	1940	1950
00-1 1-9000	C A G A C A T A A T	A A A G G A A G C T	A A A G G G A A A G
99-1 1-9000	C A G A G A T A A T	T A A G G A A G C C	A A G G G A A A A G

Figure 53 cont'd

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		1960		1970		1980
00-1 1-9000	C A G C A G A A A T		G A T G G A A G A G		G A A A T G A G T C	
99-1 1-9000	C A G C T G A A A T		G A T G G A A G A A		G A G A T G A A T C	
		1990		2000		2010
00-1 1-9000	A A C G A T C A A A		A A T A G G A A A T		G G T A G T G T A A	
99-1 1-9000	A A A G A T C A A A		A A T A G G A A A T		G G C A G T G T A A	
		2020		2030		2040
00-1 1-9000	A A T T A A C A G A		A A A A G C A A A A		G A G C T C A A C A	
99-1 1-9000	A A C T A A C C G A		G A A G G C A A A A		G A G C T C A A C A	
		2050		2060		2070
00-1 1-9000	A A A T T G T T G A		A G A T G A A A G C		A C A A G T G G A G	
99-1 1-9000	A A A T T G T T G A		A G A C G A G A G C		A C A A G C G G T G	
		2080		2090		2100
00-1 1-9000	A A T C C G A A G A		A G A A G A A G A A		C C A A A A G A C A	
99-1 1-9000	A A T C A G A A G A		A G A A G A A G A A		C C A A A A G A A A	
		2110		2120		2130
00-1 1-9000	C A C A A G A C A A		T A G T C A A G A A		G A T G A C A T T T	
99-1 1-9000	C T C A G G A T A A		C A A T C A A G G A		G A A G A T A T T T	
		2140		2150		2160
00-1 1-9000	A C C A G T T A A T		T A T G T A G T T T		A A T A A A A A T A	
99-1 1-9000	A T C A G T T A A T		C A T G T A G T T T		A A T A A A A A T A	
		2170		2180		2190
00-1 1-9000	A A C A A T G G G A		C A A G T A A A A A		T G G A G T C C T A	
99-1 1-9000	A A C A A T G G G A		C A A G T C A A G A		T G G A G T C C T A	
		2200		2210		2220
00-1 1-9000	C C T A G T A G A C		A C C T A T C A A G		G C A T T C C T T A	
99-1 1-9000	T C T A G T A G A C		A C T T A T C A A G		G C A T T C C A T A	
		2230		2240		2250
00-1 1-9000	C A C A G C A G C T		G T T C A A G T T G		A T C T A A T A G A	
99-1 1-9000	T A C A G C T G C T		G T T C A A G T T G		A C C T G G T A G A	
		2260		2270		2280
00-1 1-9000	A A A G G A C C T G		T T A C C T G C A A		G C C T A A C A A T	
99-1 1-9000	A A A A G A T T T A		C T G C C A G C A A		G T T T G A C A A T	
		2290		2300		2310
00-1 1-9000	A T G G T T C C C T		T T G T T T C A G G		C C A A C A C A C C	
99-1 1-9000	A T G G T T T C C T		T T A T T T C A G G		C C A A C A C A C C	
		2320		2330		2340
00-1 1-9000	A C C A G C A G T G		C T G C T C G A T C		A G C T A A A A A C	
99-1 1-9000	A C C A G C A G T T		C T G C T T G A T C		A G C T A A A A A C	

Figure 53 cont'd

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00-1 1-9000	2350 CCTGACAATA	2360 ACCACTCTGT	2370 ATGCTGCATC
99-1 1-9000	CCTGACAATA	ACCACTCTGT	ATGCTGCATC
00-1 1-9000	2380 ACAAAATGGT	2390 CCAATACTCA	2400 AAGTGAATGC
99-1 1-9000	ACAGAATGGT	CCAATACTCA	AGGTAATGC
00-1 1-9000	2410 ATCAGCCCAA	2420 GGTGCGAGCA	2430 TGTCTGTACT
99-1 1-9000	ATCTGCCCAA	GGTGCTGCCA	TGTCTGTACT
00-1 1-9000	2440 TCCCCAAAAA	2450 TTTGAAGTCA	2460 ATGCGACTGT
99-1 1-9000	TCCCCAAAAA	TTCGAGGTAA	ATGCAACTGT
00-1 1-9000	2470 AGCACTCGAT	2480 GAATATAGCA	2490 AACTGGAATT
99-1 1-9000	AGCACTTGAT	GAATACAGTA	AACTTGATTT
00-1 1-9000	2500 TGACAAACTC	2510 ACAGTCTGTG	2520 AAGTAAAAAC
99-1 1-9000	TGACAAAGCTG	ACGGTCTGCG	ATGTATAAAC
00-1 1-9000	2530 AGTTTACTTA	2540 ACAACCATGA	2550 AACCATACGG
99-1 1-9000	AGTTTATTTG	ACAACCTATGA	AACCGTACGG
00-1 1-9000	2560 GATGGTATCA	2570 AAATTTGTGA	2580 GCTCAGCCAA
99-1 1-9000	GATGGTGTCA	AAATTTGTGA	GTTCAGCCAA
00-1 1-9000	2590 ATCAGTTGCG	2600 AAAAAAACAC	2610 ATGATCTAAT
99-1 1-9000	ATCAGTTGCG	AAAAAGACAC	ATGATCTAAT
00-1 1-9000	2620 CGCACTATGT	2630 GATTTTATGG	2640 ATCTAGAAAA
99-1 1-9000	TGCACTATGT	GACTTCATGG	ACCTAGAGAA
00-1 1-9000	2650 GAACACACCT	2660 GTTACAATAC	2670 CAGCATTTCAT
99-1 1-9000	AAATATACCT	GTGACAATAC	CAGCATTTCAT
00-1 1-9000	2680 CAAATCAGTT	2690 TCAATCAAAG	2700 AGAGTGAGTC
99-1 1-9000	AAAGTCAGTT	TCAATCAAAG	AGAGTGAATC
00-1 1-9000	2710 AGCTACTGTT	2720 GAAGCTGCTA	2730 TAAGCAGTGA
99-1 1-9000	AGCCACTGTT	GAAGCTGCAA	TAAGCAGCGA

Figure 53 cont'd

WO 03/072719		PCT/US03/05271	
00-1 1-9000	AGCAGACCAA	GCCTTAACAC	AGGCCAAAT
99-1 1-9000	AGCCGACCAA	GCCTTGACAC	AAGCCAAGAT
00-1 1-9000	TGCACCTTAT	GCGGGATTAA	TTATGATCAT
99-1 1-9000	TGCGCCCTAT	GCAGGACTAA	TTATGATCAT
00-1 1-9000	GACTATGAAC	AATCCCAAAG	GCATATTCAA
99-1 1-9000	GACCATGAAC	AATCCCAAAG	GTATATTCAA
00-1 1-9000	AAAGCTTGA	GCTGGGACTC	AAGTCATAGT
99-1 1-9000	GAAACTAGGG	GCTGGAAACAC	AAGTGATAGT
00-1 1-9000	AGAACTAGGA	GCATATGTCC	AGGCTGAAAG
99-1 1-9000	AGAGCTGGGG	GCATATGTTC	AGGCTGAGAG
00-1 1-9000	CATAAGCAAA	ATATGCAAGA	CTTGGAGCCA
99-1 1-9000	CATCAGTAGG	ATCTGCAAGA	GCTGGAGTCA
00-1 1-9000	TCAAGGGACA	AGATATGTCT	TGAAGTCCAG
99-1 1-9000	CCAAGGAACA	AGATACGTAC	TAAATCCAG
00-1 1-9000	ATAACAACCA	AGCACCTTGG	CCAAGAGCTA
99-1 1-9000	ATAA - AAATA	ACTGTCTTAA	TCAATAATTG
00-1 1-9000	CTAACCCCTAT	CTCATAGATC	A - TAAAGTCA
99-1 1-9000	CTTATATAAC	TCTAGAGATT	AATAAGCTTA
00-1 1-9000	CCATTCTAGT	TATATAAAAA	TCAAGTTAGA
99-1 1-9000	TTATTATAGT	TATATAAAAA	T - AAATTAGA
00-1 1-9000	ACAAGAATTA	AATCAATCAA	GAACGGGACA
99-1 1-9000	ATTAGAAGGG	CATCAATAGA	AAGCGGGACA
00-1 1-9000	AATAAAAATG	TCTTGGAAG	TGGTGATCAT
99-1 1-9000	AATAAAAATG	TCTTGGAAG	TGATGATCAT
00-1 1-9000	TTTTTCATTG	TTAATAACAC	CTCAACACGG
99-1 1-9000	CATTTTCGTTA	CTCATAACAC	CCCAGCACGG

Figure 53 cont'd

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	3130	98/132	3140	3150
00-1 1-9000	TCTTAAAGAG	AGCTACTTAG	AAGAGTTCATG	
99-1 1-9000	GCTAAAGGAG	AGTTATTTGG	AAGAATCATG	
	3160	3170	3180	
00-1 1-9000	TAGCACTATA	ACTGAAGGAT	ATCTCAGTGT	
99-1 1-9000	TAGTACTATA	ACTGAGGGAT	ACCTCAGTGT	
	3190	3200	3210	
00-1 1-9000	TCTGAGGACA	GGTTGGGTACA	CCAATGTTTT	
99-1 1-9000	TTTAAGAACAA	GGCTGGGTACA	CTAATGTCCT	
	3220	3230	3240	
00-1 1-9000	TACACTGGAG	GTAGGCGGATG	TAGAGAACCT	
99-1 1-9000	CACATTAGAA	GTTGGGTGATG	TTGAAAATCT	
	3250	3260	3270	
00-1 1-9000	TACATGTGCC	GATGGACCCA	GCTTAATAAA	
99-1 1-9000	TACATGTACT	GATGGACCTA	GCTTAATCAA	
	3280	3290	3300	
00-1 1-9000	AACAGAATTA	GACCTGACCA	AAAGTGCACT	
99-1 1-9000	AACAGAACTT	GATCTAACA	AAAGTGCTTT	
	3310	3320	3330	
00-1 1-9000	AAGAGAGCTC	AGAACAGTTT	CTGCTGATCA	
99-1 1-9000	AAGGGAAGCTC	AAACAGTCT	CTGCTGATCA	
	3340	3350	3360	
00-1 1-9000	ACTGGCAAGA	GAGGAGCAAA	TTGAAAATCC	
99-1 1-9000	GTTGGCGAGA	GAGGAGCAAA	TTGAAAATCC	
	3370	3380	3390	
00-1 1-9000	CAGACAATCT	AGATTCTGTTT	TAGGAGCAAT	
99-1 1-9000	CAGACAATCA	AGATTTGTCT	TAGGTGCGAT	
	3400	3410	3420	
00-1 1-9000	AGCACTCGGT	GTTGCAACTG	CAGCTGCAGT	
99-1 1-9000	AGCTCTCGGA	GTTGCTACAG	CAGCAGCAGT	
	3430	3440	3450	
00-1 1-9000	TACAGCAGGT	GTTGCAATTG	CCAAAACCAT	
99-1 1-9000	CACAGCAGGC	ATTGCAATAG	CCAAAACCAT	
	3460	3470	3480	
00-1 1-9000	CCGGCTTTGAA	AGTGAAGTAA	CAGCAATTAA	
99-1 1-9000	AAGGCTTTGAG	AGTGAGGTGA	ATGCAATTAA	
	3490	3500	3510	
00-1 1-9000	GAATGCCCTC	AAAAAGACCA	ATGAAGCAGT	
99-1 1-9000	AGGTGCTCTC	AAACAATACTA	ATGAAGCAGT	

Figure 53 cont'd

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	3520	99/132 3530	3540
00-1 1-9000	ATCTACATTG	GGGAATGGAG	TTCGTGTGTT
99-1 1-9000	ATCCACATTA	GGGAATGGTG	TGCGGGTCCT
	3550	3560	3570
00-1 1-9000	GGCAACTGCA	GTGAGAGAGC	TGAAAGATT
99-1 1-9000	AGCCACTGCA	GTGAGAGAGC	TAAAGAATT
	3580	3590	3600
00-1 1-9000	TGTGAGCAAG	AATCTAACAC	GTGCAATCAA
99-1 1-9000	TGTGAGCAAA	AACCTGACTA	GTGCAATCAA
	3610	3620	3630
00-1 1-9000	CAAAACAAG	TGCGACATTG	CTGACCTGAA
99-1 1-9000	CAGGAACAAA	TGTGACATTG	CTGATCTGAA
	3640	3650	3660
00-1 1-9000	AATGGCCGTT	AGCTTTCAGTC	AATTCAACAG
99-1 1-9000	GATGGCTGTC	AGCTTTCAGTC	AATTCAACAG
	3670	3680	3690
00-1 1-9000	AAGGTTCTTA	AATGTTGTGC	GGCAATTTTC
99-1 1-9000	AAGATTCTTA	AATGTTGTGC	GGCAGTTTTC
	3700	3710	3720
00-1 1-9000	AGACAACGCT	GGATAAACAC	CAGCAATATC
99-1 1-9000	AGACAATGCA	GGATAAACAC	CAGCAATATC
	3730	3740	3750
00-1 1-9000	TTTGGACTTA	ATGACAGATG	CTGAAGTAGC
99-1 1-9000	ATTGGACCTG	ATGACTGATG	CTGAGTTGGC
	3760	3770	3780
00-1 1-9000	CAGAGCTGTT	TCCAACATGC	CAACATCTGC
99-1 1-9000	CAGAGCTGTA	TCATACATGC	CAACATCTGC
	3790	3800	3810
00-1 1-9000	AGGACAAATA	AAACTGATGT	TGGAGAACCG
99-1 1-9000	AGGGCAGATA	AAACTGATGT	TGGAGAACCG
	3820	3830	3840
00-1 1-9000	TGCAATGGTA	AGAAGAAAAG	GGTTCGGATT
99-1 1-9000	CGCAATGGTA	AGGAGAAAAG	GATTTGGAAT
	3850	3860	3870
00-1 1-9000	CCTGATAGGA	GTTTACGGAA	GCTCCGTAAT
99-1 1-9000	CCTGATAGGG	GTCTACGGAA	GCTCTGTGAT
	3880	3890	3900
00-1 1-9000	TTACATGGTG	CAACTGCCAA	TCTTTGGGGT
99-1 1-9000	TTACATGGTT	CAATTGCCGA	TCTTTGGTGT

Figure 53 cont'd

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00-1 1-9000	T A T A G A C A C G	3910	C C T T G C T G G A	3920	T A G T A A A A G C	3930
99-1 1-9000	C A T A G A T A C A		C C T T G T T G G A		T C A T C A A G G C	
00-1 1-9000	A G C C C C T T C T	3940	T G T T C A G G A A	3950	A A A A G G G A A A	3960
99-1 1-9000	A G C T C C C T C T		T G C T C A G A A A		A A A A C G G G A A	
00-1 1-9000	C T A T G C T T G C	3970	C T C T T A A G A G	3980	A A G A C C A A G G	3990
99-1 1-9000	T T A T G C T T G C		C T C C T A A G A G		A G G A T C A A G G	
00-1 1-9000	A T G G T A T T G T	4000	C A A A A T G C A G	4010	G G T C A A C T G T	4020
99-1 1-9000	G T G G T A T T G T		A A A A A T G C A G		G A T C T A C T G T	
00-1 1-9000	T T A C T A C C C A	4030	A A T G A A A A A G	4040	A C T G T G A A A C	4050
99-1 1-9000	T T A C T A C C C A		A A T G A A A A A G		A C T G C G A A A C	
00-1 1-9000	A A G A G G A G A C	4060	C A T G T C T T T T	4070	G C G A C A C A G C	4080
99-1 1-9000	A A G A G G T G A T		C A T G T T T T T T		G T G A C A C A G C	
00-1 1-9000	A G C A G G A A T C	4090	A A T G T T G C T G	4100	A G C A G T C A A A	4110
99-1 1-9000	A G C A G G G A T C		A A T G T T G C T G		A G C A A T C A A G	
00-1 1-9000	G G A G T G C A A C	4120	A T A A A C A T A T	4130	C T A C T A C T A A	4140
99-1 1-9000	A G A A T G C A A C		A T C A A C A T A T		C T A C T A C C A A	
00-1 1-9000	T T A C C C A T G C	4150	A A A G T T A G C A	4160	C A G G A A G A C A	4170
99-1 1-9000	C T A C C C A T G C		A A A G T C A G C A		C A G G A A G A C A	
00-1 1-9000	T C C T A T C A G T	4180	A T G G T T G C A C	4190	T A T C T C C T C T	4200
99-1 1-9000	C C C T A T A A G C		A T G G T T G C A C		T A T C A C C T C T	
00-1 1-9000	T G G G G C T T T G	4210	G T T G C T T G C T	4220	A C A A G G G A G T	4230
99-1 1-9000	C G G T G C T T T G		G T G G C T T G C T		A T A A A G G G G T	
00-1 1-9000	G A G C T G T T C C	4240	A T T G G C A G C A	4250	A C A G A G T A G G	4260
99-1 1-9000	A A G C T G C T C G		A T T G G C A G C A		A T T G G G T T G G	
00-1 1-9000	G A T C A T C A A G	4270	C A A C T G A A C A	4280	A A G G C T G C T C	4290
99-1 1-9000	A A T C A T C A A A		C A A T T A C C C A		A A G G C T G C T C	

Figure 53 cont'd

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	4300	4310	4320
00-1 1-9000	T T A T A T A A C C	A A C C A A G A C G	C A G A C A C A G T
99-1 1-9000	A T A C A T A A C C	A A C C A G G A T G	C A G A C A C T G T
	4330	4340	4350
00-1 1-9000	G A C A A T A G A C	A A C A C T G T A T	A C C A G C T A A G
99-1 1-9000	A A C A A T T G A C	A A T A C C G T G T	A T C A A C T A A G
	4360	4370	4380
00-1 1-9000	C A A A G T T G A A	G G C G A A C A G C	A T G T T A T A A A
99-1 1-9000	C A A A G T T G A A	G G T G A A C A G C	A T G T A A T A A A
	4390	4400	4410
00-1 1-9000	A G G A A G G C C A	G T G T C A A G C A	G C T T T G A C C C
99-1 1-9000	A G G G A G A C C A	G T T T C A A G C A	G T T T T G A T C C
	4420	4430	4440
00-1 1-9000	A G T C A A G T T T	C C T G A A G A T C	A A T T C A A T G T
99-1 1-9000	A A T C A A G T T T	C C T G A G G A T C	A G T T C A A T G T
	4450	4460	4470
00-1 1-9000	T G C A C T T G A C	C A A G T T T T C G	A G A G C A T T G A
99-1 1-9000	T G C G C T T G A T	C A A G T C T T C G	A A A G C A T T G A
	4480	4490	4500
00-1 1-9000	G A A C A G T C A G	G C C T T G G T G G	A T C A A T C A A A
99-1 1-9000	G A A C A G T C A G	G C A C T A G T G G	A C C A G T C A A A
	4510	4520	4530
00-1 1-9000	C A G A A T C C T A	A G C A G T G C A G	A G A A A G G A A A
99-1 1-9000	C A A A A T T C T A	A A C A G T G C A G	A A A A A G G A A A
	4540	4550	4560
00-1 1-9000	C A C T G G C T T C	A T C A T T G T A A	T A A T T C T A A T
99-1 1-9000	C A C T G G T T T C	A T T A T C G T A G	T A A T T T T G G T
	4570	4580	4590
00-1 1-9000	T G C T G T C C T T	G G C T C T A C C A	T G A T C C T A G T
99-1 1-9000	T G C T G T T C T T	G G T C T A A C C A	T G A T T T C A G T
	4600	4610	4620
00-1 1-9000	G A G T G T T T T T	A T C A T A A T A A	A G A A A C A A A A
99-1 1-9000	G A G C A T C A T C	A T C A T A A T C A	A G A A A C A A A G
	4630	4640	4650
00-1 1-9000	G A A A C C C A C A	G G A G C A C C T C	C A G A G C T G A G
99-1 1-9000	G A A G C C C A C A	G G A G C A C C T C	C A G A G C T G A A
	4660	4670	4680
00-1 1-9000	T G G T G T C A C A	A A C A A T G G C T	T C A T A C C A C A
99-1 1-9000	T G G T G T C A C C	A A C G G C G G T T	T C A T A C C A C A

Figure 53 cont'd

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	4690	4700	4710
00-1 1-9000	T A A T T A G T T A	A T T A A A A A T A	A A G T A A A T T A
99-1 1-9000	T A G T T A G T T A	A T T A A A A A - -	- - - - A - - - -
	4720	4730	4740
00-1 1-9000	A A A T A A A T T A	A A A T T A A A A A	T A A A A A T T T G
99-1 1-9000	- - - - -	- - - - -	- - - - - T G
	4750	4760	4770
00-1 1-9000	G G A C A A A T C A	T A A T G T C T C G	C A A G G C T C C G
99-1 1-9000	G G A C A A A T C A	T C A T G T C T C G	T A A G G C T C C A
	4780	4790	4800
00-1 1-9000	T G C A A A T A T G	A A G T G C G G G G	C A A A T G C A A T
99-1 1-9000	T G C A A A T A T G	A A G T G C G G G G	C A A A T G C A A C
	4810	4820	4830
00-1 1-9000	A G A G G A A G T G	A G T G C A A G T T	T A A C C A C A A T
99-1 1-9000	A G A G G G A G T G	A T T G C A A A T T	C A A T C A C A A T
	4840	4850	4860
00-1 1-9000	T A C T G G A G T T	G G C C A G A T A G	A T A C T T A T T A
99-1 1-9000	T A C T G G A G T T	G G C C T G A T A G	A T A T T T A T T G
	4870	4880	4890
00-1 1-9000	A T A A G A T C A A	A T T A T T T A T T	A A A T C A A C T T
99-1 1-9000	T T A A G A T C A A	A T T A T C T C T T	A A A T C A G C T T
	4900	4910	4920
00-1 1-9000	T T A A G G A A C A	C T G A T A G A G C	T G A T G G C T T A
99-1 1-9000	T T A A G A A A C A	C A G A T A A G G C	T G A T G G T T T G
	4930	4940	4950
00-1 1-9000	T C A A T A A T A T	C A G G A G C A G G	C A G A G A A G A T
99-1 1-9000	T C A A T A A T A T	C A G G A G C A G G	T A G A G A A G A T
	4960	4970	4980
00-1 1-9000	A G G A C A C A A G	A T T T T G T C C T	A G G T T C C A C C
99-1 1-9000	A G A A C T C A A G	A C T T T G T T C T	T G G T T C T A C T
	4990	5000	5010
00-1 1-9000	A A T G T G G T T C	A A G G T T A T A T	T G A T G A T A A C
99-1 1-9000	A A T G T G G T T C	A A G G G T A C A T	T G A T G A C A A C
	5020	5030	5040
00-1 1-9000	C A A A G C A T A A	C A A A A G C T G C	A G C C T G T T A C
99-1 1-9000	C A A G G A A T A A	C C A A G G C T G C	A G C T T G C T A T
	5050	5060	5070
00-1 1-9000	A G T C T A C A T A	A T A T A A T C A A	A C A A C T A C A A
99-1 1-9000	A G T C T A C A C A	A C A T A A T C A A	G C A A C T A C A A

Figure 53 cont'd

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	5080	5090	5100
00-1 1-9000	G A A G T T G A A G	T T A G G C A G G C	T A G A G A T A A C
99-1 1-9000	G A A A C A G A A G	T A A G A C A G G C	T A G A G A C A A C
	5110	5120	5130
00-1 1-9000	A A A C T A T C T G	A C A G C A A A C A	T G T A G C A C T T
99-1 1-9000	A A G C T T T C T G	A T A G C A A A C A	T G T G G C G C T C
	5140	5150	5160
00-1 1-9000	C A C A A C T T A G	T C C T A T C T T A	T A T G G A G A T G
99-1 1-9000	C A C A A C T T G A	T A T T A T C C T A	T A T G G A G A T G
	5170	5180	5190
00-1 1-9000	A G C A A A A C T C	C T G C A T C T T T	A A T C A A C A A T
99-1 1-9000	A G C A A A A C T C	C T G C A T C T C T	A A T C A A C A A C
	5200	5210	5220
00-1 1-9000	C T C A A G A G A C	T G C C G A G A G A	G A A A C T G A A A
99-1 1-9000	C T A A A G A A A C	T A C C A A G G G A	A A A A C T G A A G
	5230	5240	5250
00-1 1-9000	A A A T T A G C A A	A G C T C A T A A T	T G A C T T A T C A
99-1 1-9000	A A A T T A G C A A	G A T T A A T A A T	T G A T T T A T C A
	5260	5270	5280
00-1 1-9000	G C A G G T G C T G	A A A A T G A C T C	T T C A T A T G C C
99-1 1-9000	G C A G G A A C T G	A C A A T G A C T C	T T C A T A T G C C
	5290	5300	5310
00-1 1-9000	T T G C A A G A C A	G T G A A A G C A C	T A A T C A A G T G
99-1 1-9000	T T G C A A G A C A	G T G A A A G C A C	T A A T C A A G T G
	5320	5330	5340
00-1 1-9000	C A G T G A G C A T	G G T C C A G T T T	T C A T T A C T A T
99-1 1-9000	C A G T A A A C A T	G G T C C C A A A T	T C A T T A C C A T
	5350	5360	5370
00-1 1-9000	A G A G G T T G A T	G A C A T G A T A T	G G A C T C A C A A
99-1 1-9000	A G A G G C A G A T	G A T A T G A T A T	G G A C T C A C A A
	5380	5390	5400
00-1 1-9000	G G A C T T A A A A	G A A G C T T T A T	C T G A T G G G A T
99-1 1-9000	A G A A T T A A A A	G A A A C A C T G T	C T G A T G G G A T
	5410	5420	5430
00-1 1-9000	A G T G A A G T C T	C A T A C T A A C A	T T T A C A A T T G
99-1 1-9000	A G T A A A A T C A	C A C A C C A A T A	T T T A T A G T T G
	5440	5450	5460
00-1 1-9000	T T A T T T A G A A	A A C A T A G A A A	T T A T A T A T G T
99-1 1-9000	T T A C T T A G A A	A A T A T A G A A A	T A A T A T A T G T

Figure 53 cont'd

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	5470	5480	5490
00-1 1-9000	CAAGGCTTAC	TTAAGTTAGT	AAAAAC - - AC
99-1 1-9000	TAAAACTTAC	TTAAGTTAGT	AAAAAATAAA
	5500	5510	5520
00-1 1-9000	ATCAGAGTGG	GATAAATGAC	AATGATAACA
99-1 1-9000	AATAGAAATGG	GATAAATGAC	AATGAAACA
	5530	5540	5550
00-1 1-9000	TTAGATGTCA	TTAAAAGTGA	TGGGTCTTCA
99-1 1-9000	TTAGATGTCA	TAAAAGTGA	TGGATCCTCA
	5560	5570	5580
00-1 1-9000	AAACATGTA	CTCACCTCAA	AAAAATAATT
99-1 1-9000	GAAACGTGTA	ATCAACTCAA	AAAAATAATA
	5590	5600	5610
00-1 1-9000	AAAGACCACT	CTGGTAAAGT	GCTTATTGTA
99-1 1-9000	AAAAAACACT	CAGGTAAAGT	GCTTATTGCA
	5620	5630	5640
00-1 1-9000	CTTAAGTTAA	TATTAGCTTT	ACTAACATTT
99-1 1-9000	CTAAAACCTGA	TATTGGCCTT	ACTGACATTT
	5650	5660	5670
00-1 1-9000	CTCACAGTAA	CAATCACCAT	CAATTATATA
99-1 1-9000	TTCACAGCAA	CAATCACTGT	CAACTATATA
	5680	5690	5700
00-1 1-9000	AAAGTGGAAA	ACAATCTGCA	AATATGCCAG
99-1 1-9000	AAAGTAGAAA	ACAATTTGCA	GGCATGTCAA
	5710	5720	5730
00-1 1-9000	TCAA-AA-CTG	AATCAGACAA	AAAGGACTCA
99-1 1-9000	CCAAAAAATG	AATCAGACAA	AAAGGTCACA
	5740	5750	5760
00-1 1-9000	TCATCAAATA	CCACATCAGT	CACAACCAAG
99-1 1-9000	AAGCCAAATA	CCACATCAAC	AACAATCAGA
	5770	5780	5790
00-1 1-9000	ACTACTCTAA	ATCATGATAT	CACACAGTAT
99-1 1-9000	CCCACACCCG	ATCCAACCTGT	AGTACATCAT
	5800	5810	5820
00-1 1-9000	TTTAAAGTTT	TGATTCAAAG	GTATACAAAC
99-1 1-9000	TTGAAAAGGC	TGATTCAAG	ACACACCAAC
	5830	5840	5850
00-1 1-9000	TCTG - - CAA	TAAACAGTGA	CACATGCTGG
99-1 1-9000	TCTGTCACAA	AAGACAGCGA	TACTTGTGG

Figure 53 cont'd

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	5860	5870	5880
00-1 1-9000	A A A A T A A A C A	G A A A T C A A T G	C A C A A A T A T A
99-1 1-9000	A G A A T A C A C A	A G A A T C A A C G	T A C A A A T A T A
	5890	5900	5910
00-1 1-9000	A C A A C A T A C A	A A T T T T T A T G	T T T T A A A T C T
99-1 1-9000	A A A A T A T A C A	A G T T C T T A T G	C T C T G G G T T C
	5920	5930	5940
00-1 1-9000	G A A G A C A C A A	A A A C C A A C A A	T T G T G A T A A A
99-1 1-9000	A C A A A T T C A A	A A G G T A C A G A	T T G T G A G G A A
	5950	5960	5970
00-1 1-9000	C T G A C A G A T T	T A T G C A G A A A	C A A A C C A A A A
99-1 1-9000	C C A A C A G C C C	T A T G C G A C A A	A A A G T T A A A A
	5980	5990	6000
00-1 1-9000	C C A G C A G T T G	G A G T G T A T C A	C A T A G T A G A A
99-1 1-9000	A C C A T A G T A G	A A A A A C A T A G	A A A A G C A G A A
	6010	6020	6030
00-1 1-9000	T G C C A T T G T A	T A T A C A C A G T	T A A A T G G A A G
99-1 1-9000	T G T C A C T G T C	T A C A T A C A A C	C G A G T G G G G G
	6040	6050	6060
00-1 1-9000	T G C T A T C A T T	A C C C A A C C G A	T G A A A C C C A A
99-1 1-9000	T G C C T T C A T C	C C T A A A A T - -	- - - A A C A C G G
	6070	6080	6090
00-1 1-9000	T C C T A A A T G T	T A A C A C C A G A	T T A G G A T C C A
99-1 1-9000	C T T T C A A C A T	T A A A A T C A G A	A C A A C C T C C A
	6100	6110	6120
00-1 1-9000	T C C A A G T C T G	T T A G T T C A A C	A A T T T A G T T A
99-1 1-9000	C C C A G G T C T A	T C A A T A C A G T	G G T T T A G C C A
	6130	6140	6150
00-1 1-9000	T T T A A A A A T A	T T T T G A A A A C	A A G T A A G T T T
99-1 1-9000	T T T A A A A A - -	- - C C G A A T A T	T A T C T A G G C T
	6160	6170	6180
00-1 1-9000	C T A T G A T A C T	T C A T A A T A A T	A A G T A A T A A T
99-1 1-9000	G C A C G A C A C T	T T G C A A T A A T	A T G C A A T A G T
	6190	6200	6210
00-1 1-9000	T A A T T G C T T A	A T C A T C A T C A	C A A C A T T A T T
99-1 1-9000	C A A T A G T T A A	A C C A C T G C T G	C A A A C T C A T C
	6220	6230	6240
00-1 1-9000	C G A A A C C A T A	A C T A T T C A A T	T T A A A A A G T A
99-1 1-9000	C A T A A T - A T A	A T C A C T G A G T	- - - - A A T A C

Figure 53 cont'd

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	6250	6260	6270
00-1 1-9000	A A A A C A A T A	A C A T G G G A C A	A G T A G T T A T G
99-1 1-9000	A A A A T C A A G A	A A A T G G G A C A	A G T G G C T A T G
	6280	6290	6300
00-1 1-9000	G A G G T G A A A G	T G G A G A A C A T	T C G A A C A A T A
99-1 1-9000	G A A G T A A G A G	T G G A G A A C A T	T C G A G C G A T A
	6310	6320	6330
00-1 1-9000	G A T A T G C T C A	A A G C A A G A G T	A A A A A A T C G T
99-1 1-9000	G A C A T G T T C A	A A G C A A A G A T	A A A A A A C C G T
	6340	6350	6360
00-1 1-9000	G T G G C A C G C A	G C A A A T G C T T	T A A A A A T G C C
99-1 1-9000	A T A A G A A G C A	G C A G G T G C T A	T A G A A A T G C T
	6370	6380	6390
00-1 1-9000	T C T T T G G T C C	T C A T A G G A A T	A A C T A C A T T G
99-1 1-9000	A C A C T G A T C C	T T A T T G G A C T	A A C A G C G T T A
	6400	6410	6420
00-1 1-9000	A G T A T T G C C C	T C A A T A T C T A	T C T G A T C A T A
99-1 1-9000	A G C A T G G C A C	T T A A T A T T T T	C C T G A T C A T C
	6430	6440	6450
00-1 1-9000	A A C T A T A A A A	T G C A A A A A A A	C A C A T C T G A A
99-1 1-9000	G A T C A T G C A A	C A T T A A G A A A	C A T G A T C A A A
	6460	6470	6480
00-1 1-9000	T C A G A A C A T C	A C A C C A G C T C	A T C A C C C A T G
99-1 1-9000	A C A G A A A A C T	G T G C T A A C A T	G C C G T C G G C A
	6490	6500	6510
00-1 1-9000	G A A T C C A G C A	G A G A A A C T C C	A A C G G T C C C C
99-1 1-9000	G A A C C A A G C A	A A A A G A C C C C	A A T G A C C T C C
	6520	6530	6540
00-1 1-9000	A C A G A C A A C T	C A G A C A C C A A	C T C A A G C C C A
99-1 1-9000	A C A G C A G G C C	C A A A C A C C A A	A C C C A A T C C A
	6550	6560	6570
00-1 1-9000	C A G C A T C C A A	C T C A A C A G T C	C A C A G A A G G C
99-1 1-9000	C A G C A A G C A A	C A C A G T G G A C	C A C A G A G A A C
	6580	6590	6600
00-1 1-9000	T C C A C A C T C T	A C T T T G C A G C	C T C A G C A A G C
99-1 1-9000	T C A A C A T C C C	C A G T A G C A A C	C C C A G A G G G C
	6610	6620	6630
00-1 1-9000	T C A C C A G A G A	C A G A A C C A A C	A T C A A C A C C A
99-1 1-9000	C A T C C A T A C A	C A G G G A C A A C	T C A A A C A T C A

Figure 53 cont'd

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00-1 1-9000	6640 G A T A C A A C A A	6650 A C C G C C C G C C	6660 C T T C G T C G A C
99-1 1-9000	G A C A C A A C A G	C T C C C C A G C A	A A C C A C A G A C
00-1 1-9000	6670 A C A C A C A C A A	6680 C A C C A C C A A G	6690 C G C A A G C A G A
99-1 1-9000	A A A C A C A C A G	C A C C G C T A A A	A T C A A C C A A T
00-1 1-9000	6700 A C A A A G A C A A	6710 G T C C G G C A G T	6720 C - C A C A C A A A
99-1 1-9000	G A A C A G A T C A	C C C A G A C A A C	C A C A G A G A A A
00-1 1-9000	6730 A A - A C A A C C C	6740 A A G G A C A A G C	6750 T C T A G A A C A C
99-1 1-9000	A A G A C A A T C A	G A G C A A C A A C	C C A A A A A A G G
00-1 1-9000	6760 - - - - - A T	6770 T C T C C A C C A C	6780 G G G C - - A A C G
99-1 1-9000	G A A A A A G G A A	A A G A A A A C A C	A A A C C A A A C C
00-1 1-9000	6790 A C A A G G A C G G	6800 C - - - A C G C A	6810 G A - - A C C A C C
99-1 1-9000	A C A A G C A C A G	C T G C A A C C C A	A A C A A C C A A C
00-1 1-9000	6820 A C T C T C C G C A	6830 C A A G C A G C A C	6840 A A G A A A G A G A
99-1 1-9000	A C C A C C A A C C	A A A T C A G A A A	T G C A A G T G A G
00-1 1-9000	6850 C C G T C C A C A G	6860 C A T C A G T C C A	6870 A C C T G A C A T C
99-1 1-9000	A C A A T C A C A A	C A T C C G A C A G	A C C C A G A A C T
00-1 1-9000	6880 A G C G C A A C A A	6890 C C C A C A A A A A	6900 C G A A G A A G C A
99-1 1-9000	G A C A C C A C A A	C C C A A A G C A G	C G A A C A G A C A
00-1 1-9000	6910 A G T C C A G C G A	6920 G C C C A C A A A C	6930 A T C T G C A A G C
99-1 1-9000	A - C C C G G G C A	A C A G A C C C A A	G C T C C C C A C C
00-1 1-9000	6940 A C A A C A A G A A	6950 T A C A A A G G A A	6960 A A G C G T G G A G
99-1 1-9000	A C A C C A T G C A	T A G A G A G G T G	C A A A A C T C A A
00-1 1-9000	6970 G C C A A C A C A T	6980 C A - A C A A - C A	6990 T A C A A C C A A A
99-1 1-9000	A T G A G C A C A A	C A C A C A A A C A	T C C C A T C C A A
00-1 1-9000	7000 C T A G T T A A C A	7010 A A A A A T - A C A	7020 A A A T A A C T C T
99-1 1-9000	G T A G T T A A C A	A A A A A C C A C A	A A A T A A C C T T

Figure 53 cont'd

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00-1 1-9000	7030 A A G A T A A A C C	7040 A T G C A G A C A C	7050 C A A C A A T G G A
99-1 1-9000	G A - - - A A A C C	A - - - - - A -	- - - - - A - -
00-1 1-9000	7060 G A A G C C A A A A	7070 G A C A A T T C A C	7080 A A T C T C C C C A
99-1 1-9000	- A A A C C A A A A	C A T A A A C C C A	G A - - - - C C C A
00-1 1-9000	7090 A A A A G G C A A C	7100 A A C A C C A T A T	7110 T A - - - G C T C T
99-1 1-9000	G A A A A A C A T A	G A C A C C A T A T	G G A A G G T T C T
00-1 1-9000	7120 G C C C A A A T C T	7130 C C C T G G A A A A	7140 A A C A C T C G C C
99-1 1-9000	A G C A T A T G C A	C C A A T G A G A T	G G C A T C T G T T
00-1 1-9000	7150 C A T A T A C C A A	7160 A A A T A C C A C A	7170 A C C A C C C C A A
99-1 1-9000	C A T G T A T C A A	T A G C A C C A C C	A T C A T T C A A G
00-1 1-9000	7180 G A A A A A A A C T	7190 G G G C A A A A C A	7200 A C A C C C A A G A
99-1 1-9000	G A A T A A G A A G	A G G C G A A A - -	- - A T T T A A G G
00-1 1-9000	7210 G A C A A A T A A C	7220 A A T G G A T C C T	7230 C T C A A T G A A T
99-1 1-9000	G A T A A A T G A C	A A T G G A T C C C	T T T T G T G A A T
00-1 1-9000	7240 C C A C T G T T A A	7250 T G T C T A T C T T	7260 C C T G A C T C A T
99-1 1-9000	C T A C T G T T A A	T G T T T A T C T C	C C T G A T T C A T
00-1 1-9000	7270 A T C T T A A A G G	7280 A G T G A T T T T C C	7290 T T T A G T G A G A
99-1 1-9000	A T C T C A A A G G	A G T A A T A T C T	T T T A G T G A A A
00-1 1-9000	7300 C T A A T G C A A T	7310 T G G T T C A T G T	7320 C T C T T A A A A A
99-1 1-9000	C C A A T G C A A T	T G G A T C A T G T	C T T T T G A A A A
00-1 1-9000	7330 G A C C T T A C C T	7340 A A A A A A T G A C	7350 A A C A C T G C A A
99-1 1-9000	G A C C C T A T C T	A A A A A A T G A C	A A C A C T G C C A
00-1 1-9000	7360 A A G T T G C C A T	7370 A G A G A A T C C T	7380 G T T A T C G A G C
99-1 1-9000	A A G T T G C T G T	A G A A A A C C C T	G T T G T T G A A C
00-1 1-9000	7390 A T G T T A G A C T	7400 C A A A A A T G C A	7410 G T C A A T T C T A
99-1 1-9000	A T G T G A G G C T	T A G A A A T G C A	G T C A T G A C C A

Figure 53 cont'd

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00-1 1-9000	7420 A G A T G A A A A T	7430 A T C A G A T T A C	7440 A A G A T A G T A G
99-1 1-9000	A A A T G A A G A T	A T C A G A T T A T	A A A G T G G T T G
00-1 1-9000	7450 A G C C A G T A A A	7460 C A T G C A A C A T	7470 G A A A T T A T G A
99-1 1-9000	A A C C A G T T A A	T A T G C A G C A T	G A A A T A A T G A
00-1 1-9000	7480 A G A A T G T A C A	7490 C A G T T G T G A G	7500 C T C A C A T T A T
99-1 1-9000	A A A A T A T A C A	T A G T T G T G A G	C T T A C A T T A T
00-1 1-9000	7510 T A A A A C A G T T	7520 T T T A A C A A G G	7530 A G T A A A A A T A
99-1 1-9000	T A A A A C A A T T	C T T A A C G A G A	A G C A A A A A C A
00-1 1-9000	7540 T T A G C A C T C T	7550 C A A A T T A A A T	7560 A T G A T A T G T G
99-1 1-9000	T T A G C T C T C T	A A A A T T A A A T	A T G A T A T G T G
00-1 1-9000	7570 A T T G G C T G C A	7580 G T T A A A G T C T	7590 A C A T C A G A T G
99-1 1-9000	A T T G G T T A C A	G T T A A A A T C C	A C T T C A G A T A
00-1 1-9000	7600 A T A C C T C A A T	7610 C C T A A G T T T T	7620 A T A G A T G T A G
99-1 1-9000	A C A C A T C A A T	T C T C A A T T T T	A T A G A T G T G G
00-1 1-9000	7630 A A T T T A T A C C	7640 T A G C T G G G T A	7650 A G C A A T T G G T
99-1 1-9000	A G T T C A T A C C	C G T T T G G G T A	A G C A A T T G G T
00-1 1-9000	7660 T T A G T A A T T G	7670 G T A C A A T C T C	7680 A A C A A G T T G A
99-1 1-9000	T C A G T A A C T G	G T A T A A T C T C	A A T A A A T T A A
00-1 1-9000	7690 T T C T G G A A T T	7700 C A G G A A A G A A	7710 G A A G T A A T A A
99-1 1-9000	T C T T A G A G T T	T A G A A G A G A A	G A A G T A A T A A
00-1 1-9000	7720 G A A C T G G T T C	7730 A A T C T T G T G T	7740 A G G T C A T T G G
99-1 1-9000	G A A C T G G T T C	A A T T T T A T G T	A G A T C A C T A G
00-1 1-9000	7750 G T A A A T T A G T	7760 T T T T G T T G T A	7770 T C A T C A T A T G
99-1 1-9000	G C A A G T T A G T	T T T T A T T G T A	T C A T C T T A T G
00-1 1-9000	7780 G A T G T A T A G T	7790 C A A G A G C A A C	7800 A A A A G C A A A A
99-1 1-9000	G A T G T G T A G T	A A A A A G C A A C	A A A A G T A A A A

Figure 53 cont'd

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	7810	7820	7830
00-1 1-9000	G A G T G A G C T T	C T T C A C A T A C	A A T C A A C T G T
99-1 1-9000	G A G T G A G C T T	T T T C A C C T A T	A A C C A A C T G T
	7840	7850	7860
00-1 1-9000	T A A C A T G G A A	A G A T G T G A T G	T T A A G T A G A T
99-1 1-9000	T A A C A T G G A A	A G A T G T G A T G	T T A A G T A G A T
	7870	7880	7890
00-1 1-9000	T C A A T G C A A A	T T T T T G T A T A	T G G G T A A G C A
99-1 1-9000	T C A A T G C A A A	C T T T T G T A T A	T G G G T A A G T A
	7900	7910	7920
00-1 1-9000	A C A G T C T G A A	T G A A A A T C A A	G A A G G G C T A G
99-1 1-9000	A C A A C C T G A A	C A A A A A T C A A	G A A G G A C T A G
	7930	7940	7950
00-1 1-9000	G G T T G A G A A G	T A A T C T G C A A	G G C A T A T T A A
99-1 1-9000	G A C T T A G A A G	C A A T C T G C A A	G G T A T G T T A A
	7960	7970	7980
00-1 1-9000	C T A A T A A G C T	A T A T G A A A C T	G T A G A T T A T A
99-1 1-9000	C C A A T A A A T T	A T A T G A A A C T	G T T G A T T A C A
	7990	8000	8010
00-1 1-9000	T G C T T A G T T T	A T G T T G C A A T	G A A G G T T T C T
99-1 1-9000	T G C T A A G C C T	A T G C T G C A A T	G A A G G A T T C T
	8020	8030	8040
00-1 1-9000	C A C T T G T G A A	A G A G T T C G A A	G G C T T T A T T A
99-1 1-9000	C T C T G G T G A A	A G A G T T T G A A	G G A T T T A T T A
	8050	8060	8070
00-1 1-9000	T G A G T G A A A T	T C T T A G G A T T	A C T G A A C A T G
99-1 1-9000	T G A G T G A A A T	T C T A A A A A T T	A C T G A G C A T G
	8080	8090	8100
00-1 1-9000	C T C A A T T C A G	T A C T A G A T T T	A G A A A T A C T T
99-1 1-9000	C T C A G T T C A G	T A C T A G G T T T	A G G A A T A C T T
	8110	8120	8130
00-1 1-9000	T A T T A A A T G G	A T T A A C T G A T	C A A T T A A C A A
99-1 1-9000	T A T T G A A T G G	G T T A A C T G A A	C A A T T A T C A G
	8140	8150	8160
00-1 1-9000	A A T T A A A A A A	T A A A A A C A G A	C T C A G A G T T C
99-1 1-9000	T G T T G A A A G C	T A A G A A C A G A	T C T A G A G T T C
	8170	8180	8190
00-1 1-9000	A T G G T A C C G T	G T T A G A A A A T	A A T G A T T A T C
99-1 1-9000	T T G G A A C T A T	A T T A G A A A A C	A A C A A T T A C C

Figure 53 cont'd

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PCT/US03/05271

	8200	111/132	8210	8220
00-1 1-9000	C A A T G T A C G A	A G T T G T A C T T	A A G T T A T T A G	
99-1 1-9000	C T A T G T A C G A	A G T A G T A C T T	A A A T T A T T A G	
	8230	8240	8250	
00-1 1-9000	G A G A T A C T T T	G A G A T G T A T T	A A A T T A T T A A	
99-1 1-9000	G G G A C A C C T T	G A A A A G C A T A	A A G T T A T T A A	
	8260	8270	8280	
00-1 1-9000	T C A A T A A A A A	C T T A G A G A A T	G C T G C T G A A T	
99-1 1-9000	T T A A C A A G A A	T T T A G A A A A T	G C T G C A G A A T	
	8290	8300	8310	
00-1 1-9000	T A T A C T A T A T	A T T T A G A A T A	T T C G G T C A C C	
99-1 1-9000	T A T A T T A T A T	A T T C A G A A T T	T T T G G A C A C C	
	8320	8330	8340	
00-1 1-9000	C A A T G G T A G A	T G A A A G A G A T	G C A A T G G A T G	
99-1 1-9000	C T A T G G T A G A	T G A G A G G G A A	G C A A T G G A T G	
	8350	8360	8370	
00-1 1-9000	C T G T C A A A T T	A A A C A A T G A A	A T C A C A A A A A	
99-1 1-9000	C T G T T A A A T T	A A A C A A T G A G	A T T A C A A A A A	
	8380	8390	8400	
00-1 1-9000	T C C T T A G G T G	G G A G A G C T T G	A C A G A A C T A A	
99-1 1-9000	T T C T T A A A T T	A G A G A G T T T A	A C A G A A C T A A	
	8410	8420	8430	
00-1 1-9000	G A G G G G C A T T	C A T A T T A A G G	A T T A T C A A A G	
99-1 1-9000	G A G G A G C A T T	T A T A C T A A G A	A T T A T A A A A G	
	8440	8450	8460	
00-1 1-9000	G A T T T G T A G A	C A A C A A C A A A	A G A T G G C C C A	
99-1 1-9000	G G T T T G T A G A	C A A T A A T A A A	A G A T G G C C T A	
	8470	8480	8490	
00-1 1-9000	A A A T T A A A A A	C T T A A A A G T G	C T T A G T A A G A	
99-1 1-9000	A A A T T A A G A A	T T T A A A A G T G	C T C A G C A A A A	
	8500	8510	8520	
00-1 1-9000	G A T G G A C T A T	G T A C T T C A A A	G C A A A A A G T T	
99-1 1-9000	G A T G G G C T A T	G T A T T T C A A A	G C T A A A A G T T	
	8530	8540	8550	
00-1 1-9000	A C C C C A G T C A	A C T T G A A T T A	A G C G A A C A A G	
99-1 1-9000	A C C C T A G C C A	A C T T G A G C T A	A G T G T A C A A G	
	8560	8570	8580	
00-1 1-9000	A T T T T T T A G A	G C T T G C T G C A	A T A C A G T T T G	
99-1 1-9000	A T T T T T T A G A	A C T T G C T G C A	G T A C A A T T T G	

Figure 53 cont'd

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00-1 1-9000	8590 A A C A A G A G T T	112/132 T T C T G T C C C T	8600 G A A A A A C C A
99-1 1-9000	A G C A G G A A T T	C T C T G T A C C T	G A A A A A C C A
00-1 1-9000	8620 A C C T T G A G A T	8630 G G T A T T A A A T	8640 G A T A A A G C T A
99-1 1-9000	A C C T T G A G A T	G G T A T T A A A T	G A T A A A G C A A
00-1 1-9000	8650 T A T C A C C T C C	8660 T A A A A G A T T A	8670 A T A T G G T C T G
99-1 1-9000	T A T C A C C T C C	A A A A A A G C T A	A T A T G G T C T G
00-1 1-9000	8680 T G T A T C C A A A	8690 A A A T T A C T T A	8700 C C T G A G A A A A
99-1 1-9000	T A T A T C C A A A	A A A C T A C C T G	C C T G A A A C T A
00-1 1-9000	8710 T A A A A A A T C G	8720 A T A T C T A G A A	8730 G A G A C T T T C A
99-1 1-9000	T A A A A A A T C A	A T A T T T A G A A	G A G G C T T T C A
00-1 1-9000	8740 A T G C A A G T G A	8750 T A G T C T C A A A	8760 A C A A G A A G A G
99-1 1-9000	A T G C A A G T G A	C A G C C A A A G A	A C A A G G A G A G
00-1 1-9000	8770 T A C T A G A G T A	8780 C T A T T T G A A A	8790 G A T A A T A A A T
99-1 1-9000	T C T T A G A A T T	T T A C T T A A A A	G A T T G T A A A T
00-1 1-9000	8800 T C G A C C A A A A	8810 A G A A C T T A A A	8820 A G T T A T G T T G
99-1 1-9000	T T G A T C A A A A	A G A A C T T A A A	C G T T A T G T A A
00-1 1-9000	8830 T T A A A C A A G A	8840 A T A T T T A A A T	8850 G A T A A G G A T C
99-1 1-9000	T T A A A C A A G A	G T A T C T G A A T	G A C A A A G A C C
00-1 1-9000	8860 A T A T T G T C T C	8870 G C T A A C T G G A	8880 A A A G A A A G A G
99-1 1-9000	A C A T T G T C T C	G T T A A C T G G G	A A G G A A A G A G
00-1 1-9000	8890 A A T T A A G T G T	8900 A G G T A G A A T G	8910 T T T G C T A T G C
99-1 1-9000	A A T T A A G T G T	A G G T A G G A T G	T T T G C A A T G C
00-1 1-9000	8920 A A C C A G G A A A	8930 A C A G C G A C A A	8940 A T A C A A A T A T
99-1 1-9000	A A C C A G G A A A	A C A A A G A C A G	A T A C A G A T A T
00-1 1-9000	8950 T G G C T G A A A A	8960 A T T G T T A G C T	8970 G A T A A T A T T G
99-1 1-9000	T A G C T G A G A A	A C T T C T A G C T	G A T A A T A T T G

Figure 53 cont'd

WO 03/072719		PCT/US03/05271	
	8980	113/132	8990
00-1 1-9000	T A C C T T T T T T	C C C A G A A A C C	T T A A C A A A G T
99-1 1-9000	T A C C T T T T T T	C C C A G A A A C T	T T A A C A A A G T
	9010	9020	9030
00-1 1-9000	A T G G T G A T C T	A G A T C T T C A G	A G A A T A A T G G
99-1 1-9000	A T G G T G A C T T	A G A T C T C C A A	A G A A T T A T G G
	9040	9050	9060
00-1 1-9000	A A A T C A A A T C	G G A A C	
99-1 1-9000	A A A T A A A A T C	A G A A C T T T C T	T C C A T T A A A A
	9070	9080	9090
00-1 1-9000			
99-1 1-9000	C T A G A A A G A A	T G A T A G C T A C	A A C A A T T

Figure 53 cont'd

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00-1 7001-13350	1 10 A C A A T G G A G A	20 A G C C A A A A G A	30 C A A T T C A C A A
99-1 7001-13294	- - - - -	- - - - -	- - - - -
00-1 7001-13350	40 T C T C C C C A A A	50 A A G G C A A C A A	60 C A C C A T A T T A
99-1 7001-13294	- - - - -	- A A A C A T A G A	C A C C A T A T G G
00-1 7001-13350	70 - - - G C T C T G C	80 C C A A A T C T C C	90 C T G G A A A A A A
99-1 7001-13294	A A G G T T C T A G	C A T A T G C A C C	A A T G A G A T G G
00-1 7001-13350	100 C A C T C G C C C A	110 T A T A C C A A A A	120 A T A C C A C A A C
99-1 7001-13294	C A T C T G T T C A	T G T A T C A A T A	G C A C C A C C A T
00-1 7001-13350	130 C A C C C C A A G A	140 A A A A A A C T G G	150 G C A A A A C A A C
99-1 7001-13294	C A T T C A A G G A	A T A A G A A G A G	G C G A A A - - -
00-1 7001-13350	160 A C C C A A G A G A	170 C A A A T A A C A A	180 T G G A T C C T C T
99-1 7001-13294	A T T T A A G G G A	T A A A T G A C A A	T G G A T C C C T T
00-1 7001-13350	190 C A A T G A A T C C	200 A C T G T T A A T G	210 T C T A T C T T C C
99-1 7001-13294	T T G T G A A T C T	A C T G T T A A T G	T T T A T C T C C C
00-1 7001-13350	220 T G A C T C A T A T	230 C T T A A A G G A G	240 T G A T T T C C T T
99-1 7001-13294	T G A T T C A T A T	C T C A A A G G A G	T A A T A T C T T T
00-1 7001-13350	250 T A G T G A G A C T	260 A A T G C A A T T G	270 G T T C A T G T C T
99-1 7001-13294	T A G T G A A A C C	A A T G C A A T T G	G A T C A T G T C T
00-1 7001-13350	280 C T T A A A A A G A	290 C C T T A C C T A A	300 A A A A T G A C A A
99-1 7001-13294	T T T G A A A A G A	C C C T A T C T A A	A A A A T G A C A A
00-1 7001-13350	310 C A C T G C A A A A	320 G T T G C C A T A G	330 A G A A T C C T G T
99-1 7001-13294	C A C T G C C A A A	G T T G C T G T A G	A A A A C C C T G T
00-1 7001-13350	340 T A T C G A G C A T	350 G T T A G A C T C A	360 A A A A T G C A G T
99-1 7001-13294	T G T T G A A C A T	G T G A G G C T T A	G A A A T G C A G T
00-1 7001-13350	370 C A A T T C T A A G	380 A T G A A A A T A T	390 C A G A T T A C A A
99-1 7001-13294	C A T G A C C A A A	A T G A A G A T A T	C A G A T T A T A A

Figure 53 cont'd

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00-1 7001-13350	400 G A T A G T A G A G	410 C C A G T A A A C A	420 T G C A A C A T G A
99-1 7001-13294	A G T G G T T G A A	C C A G T T A A T A	T G C A G C A T G A
00-1 7001-13350	430 A A T T A T G A A G	440 A A T G T A C A C A	450 G T T G T G A G C T
99-1 7001-13294	A A T A A T G A A A	A A T A T A C A T A	G T T G T G A G C T
00-1 7001-13350	460 C A C A T T A T T A	470 A A A C A G T T T T	480 T A A C A A G G A G
99-1 7001-13294	T A C A T T A T T A	A A A C A A T T C T	T A A C G A G A A G
00-1 7001-13350	490 T A A A A A T A T T	500 A G C A C T C T C A	510 A A T T A A A T A T
99-1 7001-13294	C A A A A A C A T T	A G C T C T C T A A	A A T T A A A T A T
00-1 7001-13350	520 G A T A T G T G A T	530 T G G C T G C A G T	540 T A A A G T C T A C
99-1 7001-13294	G A T A T G T G A T	T G G T T A C A G T	T A A A A T C C A C
00-1 7001-13350	550 A T C A G A T G A T	560 A C C T C A A T C C	570 T A A G T T T T A T
99-1 7001-13294	T T C A G A T A A C	A C A T C A A T T C	T C A A T T T T A T
00-1 7001-13350	580 A G A T G T A G A A	590 T T T A T A C C T A	600 G C T G G G T A A G
99-1 7001-13294	A G A T G T G G A G	T T C A T A C C C G	T T T G G G T A A G
00-1 7001-13350	610 C A A T T G G T T T	620 A G T A A T T G G T	630 A C A A T C T C A A
99-1 7001-13294	C A A T T G G T T C	A G T A A C T G G T	A T A A T C T C A A
00-1 7001-13350	640 C A A G T T G A T T	650 C T G G A A T T C A	660 G G A A A G A A G A
99-1 7001-13294	T A A A T T A A T C	T T A G A G T T T A	G A A G A G A A G A
00-1 7001-13350	670 A G T A A T A A G A	680 A C T G G T T C A A	690 T C T T G T G T A G
99-1 7001-13294	A G T A A T A A G A	A C T G G T T C A A	T T T T A T G T A G
00-1 7001-13350	700 G T C A T T G G G T	710 A A A T T A G T T T	720 T T G T T G T A T C
99-1 7001-13294	A T C A C T A G G C	A A G T T A G T T T	T T A T T G T A T C
00-1 7001-13350	730 A T C A T A T G G A	740 T G T A T A G T C A	750 A G A G C A A C A A
99-1 7001-13294	A T C T T A T G G A	T G T G T A G T A A	A A A G C A A C A A
00-1 7001-13350	760 A A G C A A A A G A	770 G T G A G C T T C T	780 T C A C A T A C A A
99-1 7001-13294	A A G T A A A A G A	G T G A G C T T T T	T C A C C T A T A A

Figure 53 cont'd

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00-1 7001-13350	790 T C A A C T G T T A	800 A C A T G G A A A G	810 A T G T G A T G T T
99-1 7001-13294	C C A A C T G T T A	A C A T G G A A A G	A T G T G A T G T T
00-1 7001-13350	820 A A G T A G A T T C	830 A A T G C A A A T T	840 T T T G T A T A T G
99-1 7001-13294	A A G T A G A T T C	A A T G C A A A C T	T T T G T A T A T G
00-1 7001-13350	850 G G T A A G C A A C	860 A G T C T G A A T G	870 A A A A T C A A G A
99-1 7001-13294	G G T A A G T A A C	A A C C T G A A C A	A A A A T C A A G A
00-1 7001-13350	880 A G G G C T A G G G	890 T T G A G A A G T A	900 A T C T G C A A G G
99-1 7001-13294	A G G A C T A G G A	C T T A G A A G C A	A T C T G C A A G G
00-1 7001-13350	910 C A T A T T A A C T	920 A A T A A G C T A T	930 A T G A A A C T G T
99-1 7001-13294	T A T G T T A A C C	A A T A A A T T A T	A T G A A A C T G T
00-1 7001-13350	940 A G A T T A T A T G	950 C T T A G T T T A T	960 G T T G C A A T G A
99-1 7001-13294	T G A T T A C A T G	C T A A G C C T A T	G C T G C A A T G A
00-1 7001-13350	970 A G G T T T C T C A	980 C T T G T G A A A G	990 A G T T C G A A G G
99-1 7001-13294	A G G A T T C T C T	C T G G T G A A A G	A G T T T G A A G G
00-1 7001-13350	1000 C T T T A T T A T G	1010 A G T G A A A T T C	1020 T T A G G A T T A C
99-1 7001-13294	A T T T A T T A T G	A G T G A A A T T C	T A A A A A T T A C
00-1 7001-13350	1030 T G A A C A T G C T	1040 C A A T T C A G T A	1050 C T A G A T T T A G
99-1 7001-13294	T G A G C A T G C T	C A G T T C A G T A	C T A G G T T T A G
00-1 7001-13350	1060 A A A T A C T T T A	1070 T T A A A T G G A T	1080 T A A C T G A T C A
99-1 7001-13294	G A A T A C T T T A	T T G A A T G G G T	T A A C T G A A C A
00-1 7001-13350	1090 A T T A A C A A A A	1100 T T A A A A A A T A	1110 A A A A C A G A C T
99-1 7001-13294	A T T A T C A G T G	T T G A A A G C T A	A G A A C A G A T C
00-1 7001-13350	1120 C A G A G T T C A T	1130 G G T A C C G T G T	1140 T A G A A A A T A A
99-1 7001-13294	T A G A G T T C T T	G G A A C T A T A T	T A G A A A A C A A
00-1 7001-13350	1150 T G A T T A T C C A	1160 A T G T A C G A A G	1170 T T G T A C T T A A
99-1 7001-13294	C A A T T A C C C T	A T G T A C G A A G	T A G T A C T T A A

Figure 53 cont'd

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10-1 7001-13350	1180 G T T A T T A G G A	1190 G A T A C T T T G A	1200 G A T G T A T T A A
99-1 7001-13294	A T T A T T A G G G	G A C A C C T T G A	A A A G C A T A A A
10-1 7001-13350	1210 A T T A T T A A T C	1220 A A T A A A A A C T	1230 T A G A G A A T G C
99-1 7001-13294	G T T A T T A A T T	A A C A A G A A T T	T A G A A A A T G C
10-1 7001-13350	1240 T G C T G A A T T A	1250 T A C T A T A T A T	1260 T T A G A A T A T T
99-1 7001-13294	T G C A G A A T T A	T A T T A T A T A T	T C A G A A T T T T
10-1 7001-13350	1270 C G G T C A C C C A	1280 A T G G T A G A T G	1290 A A A G A G A T G C
99-1 7001-13294	T G G A C A C C C T	A T G G T A G A T G	A G A G G G A A G C
10-1 7001-13350	1300 A A T G G A T G C T	1310 G T C A A A T T A A	1320 A C A A T G A A A T
99-1 7001-13294	A A T G G A T G C T	G T T A A A T T A A	A C A A T G A G A T
10-1 7001-13350	1330 C A C A A A A A T C	1340 C T T A G G T G G G	1350 A G A G C T T G A C
99-1 7001-13294	T A C A A A A A T T	C T T A A A T T A G	A G A G T T T A A C
10-1 7001-13350	1360 A G A A C T A A G A	1370 G G G G C A T T C A	1380 T A T T A A G G A T
99-1 7001-13294	A G A A C T A A G A	G G A G C A T T T A	T A C T A A G A A T
10-1 7001-13350	1390 T A T C A A A G G A	1400 T T T G T A G A C A	1410 A C A A C A A A A G
99-1 7001-13294	T A T A A A A G G G	T T T G T A G A C A	A T A A T A A A A G
10-1 7001-13350	1420 A T G G C C C A A A	1430 A T T A A A A A C T	1440 T A A A A G T G C T
99-1 7001-13294	A T G G C C T A A A	A T T A A G A A T T	T A A A A G T G C T
10-1 7001-13350	1450 T A G T A A G A G A	1460 T G G A C T A T G T	1470 A C T T C A A A G C
99-1 7001-13294	C A G C A A A A G A	T G G G C T A T G T	A T T T C A A A G C
10-1 7001-13350	1480 A A A A A G T T A C	1490 C C C A G T C A A C	1500 T T G A A T T A A G
99-1 7001-13294	T A A A A G T T A C	C C T A G C C A A C	T T G A G C T A A G
10-1 7001-13350	1510 C G A A C A A G A T	1520 T T T T T A G A G C	1530 T T G C T G C A A T
99-1 7001-13294	T G T A C A A G A T	T T T T T A G A A C	T T G C T G C A G T
10-1 7001-13350	1540 A C A G T T T T G A A	1550 C A A G A G T T T T	1560 C T G T C C C T G A
99-1 7001-13294	A C A A T T T T G A G	C A G G A A T T C T	C T G T A C C T G A

Figure 53 cont'd

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	1570	1580	1590
00-1 7001-13350	A A A A A C C A A C	C T T G A G A T G G	T A T T A A A T G A
99-1 7001-13294	A A A A A C C A A C	C T T G A G A T G G	T A T T A A A T G A
	1600	1610	1620
00-1 7001-13350	T A A A G C T A T A	T C A C C T C C T A	A A A G A T T A A T
99-1 7001-13294	T A A A G C A A T A	T C A C C T C C A A	A A A A G C T A A T
	1630	1640	1650
00-1 7001-13350	A T G G T C T G T G	T A T C C A A A A A	A T T A C T T A C C
99-1 7001-13294	A T G G T C T G T A	T A T C C A A A A A	A C T A C C T G C C
	1660	1670	1680
00-1 7001-13350	T G A G A A A A T A	A A A A A T C G A T	A T C T A G A A G A
99-1 7001-13294	T G A A A C T A T A	A A A A A T C A A T	A T T T A G A A G A
	1690	1700	1710
00-1 7001-13350	G A C T T T C A A T	G C A A G T G A T A	G T C T C A A A A C
99-1 7001-13294	G G C T T T C A A T	G C A A G T G A C A	G C C A A A G A A C
	1720	1730	1740
00-1 7001-13350	A A G A A G A G T A	C T A G A G T A C T	A T T T G A A A G A
99-1 7001-13294	A A G G A G A G T C	T T A G A A T T T T	A C T T A A A A G A
	1750	1760	1770
00-1 7001-13350	T A A T A A A T T C	G A C C A A A A A G	A A C T T A A A A G
99-1 7001-13294	T T G T A A A T T T	G A T C A A A A A G	A A C T T A A A C G
	1780	1790	1800
00-1 7001-13350	T T A T G T T G T T	A A A C A A G A A T	A T T T A A A T G A
99-1 7001-13294	T T A T G T A A T T	A A A C A A G A G T	A T C T G A A T G A
	1810	1820	1830
00-1 7001-13350	T A A G G A T C A T	A T T G T C T C G C	T A A C T G G A A A
99-1 7001-13294	C A A A G A C C A C	A T T G T C T C G T	T A A C T G G G A A
	1840	1850	1860
00-1 7001-13350	A G A A A G A G A A	T T A A G T G T A G	G T A G A A T G T T
99-1 7001-13294	G G A A A G A G A A	T T A A G T G T A G	G T A G G A T G T T
	1870	1880	1890
00-1 7001-13350	T G C T A T G C A A	C C A G G A A A A C	A G C G A C A A A T
99-1 7001-13294	T G C A A T G C A A	C C A G G A A A A C	A A A G A C A G A T
	1900	1910	1920
00-1 7001-13350	A C A A A T A T T G	G C T G A A A A A T	T G T T A G C T G A
99-1 7001-13294	A C A G A T A T T A	G C T G A G A A A C	T T C T A G C T G A
	1930	1940	1950
00-1 7001-13350	T A A T A T T G T A	C C T T T T T T C C	C A G A A A C C T T
99-1 7001-13294	T A A T A T T G T A	C C T T T T T T C C	C A G A A A C T T T

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	1960	1970	1980
00-1 7001-13350	A A C A A A G T A T	G G T G A T C T A G	A T C T T C A G A G
99-1 7001-13294	A A C A A A G T A T	G G T G A C T T A G	A T C T C C A A A G
	1990	2000	2010
00-1 7001-13350	A A T A A T G G A A	A T C A A A T C G G	A A C T T T C T T C
99-1 7001-13294	A A T T A T G G A A	A T A A A A T C A G	A A C T T T C T T C
	2020	2030	2040
00-1 7001-13350	T A T T A A A A C T	A G A A G A A A T G	A T A G T T A T A A
99-1 7001-13294	C A T T A A A A C T	A G A A A G A A T G	A T A G C T A C A A
	2050	2060	2070
00-1 7001-13350	T A A T T A C A T T	G C A A G A G C A T	C C A T A G T A A C
99-1 7001-13294	C A A T T A T A T T	G C A A G G G C C T	C T A T A G T A A C
	2080	2090	2100
00-1 7001-13350	A G A T T T A A G T	A A G T T C A A C C	A A G C C T T T A G
99-1 7001-13294	A G A C T T A A G T	A A G T T C A A T C	A G G C C T T T A G
	2110	2120	2130
00-1 7001-13350	G T A T G A A A C T	A C A G C G A T C T	G T G C G G A T G T
99-1 7001-13294	A T A T G A A A C C	A C A G C T A T A T	G T G C A G A T G T
	2140	2150	2160
00-1 7001-13350	A G C A G A T G A A	C T A C A T G G A A	C A C A A A G C C T
99-1 7001-13294	A G C T G A T G A G	T T A C A T G G G A	C A C A A A G C T T
	2170	2180	2190
00-1 7001-13350	A T T C T G T T G G	T T A C A T C T T A	T C G T C C C T A T
99-1 7001-13294	A T T C T G T T G G	T T A C A T C T T A	T T G T T C C C A T
	2200	2210	2220
00-1 7001-13350	G A C A A C A A T G	A T A T G T G C C T	A T A G A C A T G C
99-1 7001-13294	G A C T A C A A T G	A T A T G T G C A T	A C A G A C A T G C
	2230	2240	2250
00-1 7001-13350	A C C A C C A G A A	A C A A A A G G T G	A A T A T G A T A T
99-1 7001-13294	A C C A C C A G A A	A C A A A A G G G G	A A T A T G A T A T
	2260	2270	2280
00-1 7001-13350	A G A T A A G A T A	G A A G A G C A A A	G T G G T T T A T A
99-1 7001-13294	A G A C A A A A T A	C A A G A G C A A A	G C G G A T T A T A
	2290	2300	2310
00-1 7001-13350	T A G A T A T C A T	A T G G G T G G T A	T T G A A G G A T G
99-1 7001-13294	C A G A T A T C A T	A T G G G A G G G A	T T G A A G G G T G
	2320	2330	2340
00-1 7001-13350	G T G T C A A A A A	C T C T G G A C A A	T G G A A G C T A T
99-1 7001-13294	G T G C C A G A A G	T T A T G G A C A A	T G G A A G C A A T

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	2350	2360	2370
10-1 7001-13350	ATCTCTATTA	GATGTTGTAT	CTGTAAAAAC
99-1 7001-13294	ATCCTTGTTA	GATGTAGTAT	CTGTGAAGAC
	2380	2390	2400
10-1 7001-13350	ACGATGTCAA	ATGACATCTT	TATTAAACGG
99-1 7001-13294	TCGCTGTCAG	ATGACCTCTC	TATTAAACGG
	2410	2420	2430
10-1 7001-13350	TGACAACCAA	TCAATAGATG	TAAGTAAACC
99-1 7001-13294	AGACAATCAG	TCAATAGATG	TTAGTAAACC
	2440	2450	2460
10-1 7001-13350	AGTTAAGTTA	TCTGAGGGTT	TAGATGAAGT
99-1 7001-13294	AGTAA AATTG	TCTGAAGGTA	TAGATGAAGT
	2470	2480	2490
10-1 7001-13350	GAAAGCAGAT	TATAGCTTGG	CTGTAAAAAT
99-1 7001-13294	AAAAGCAGAC	TATAGCTTAG	CAATTAGAAT
	2500	2510	2520
10-1 7001-13350	GTTAAAAGAA	ATAAGAGATG	CATACAGAAA
99-1 7001-13294	GCTTAAAGAA	ATAAGAGATG	CTTATAAAAA
	2530	2540	2550
10-1 7001-13350	TATAGGCCAT	AAACTTTAAAG	AAGGGGAAC
99-1 7001-13294	CATTGGTCA	AAACTCAAAG	AAGGTGAAC
	2560	2570	2580
10-1 7001-13350	ATATATATCA	AGAGATCTTC	AGTTTATAAG
99-1 7001-13294	ATATATATCA	AGGGATCTCC	AATTTATAAG
	2590	2600	2610
10-1 7001-13350	TAAGGTGATT	CAATCTGAAG	GAGTAATGCA
99-1 7001-13294	TAAGGTGATT	CAATCTGAAG	GAGTCATGCA
	2620	2630	2640
10-1 7001-13350	TCCTACCCCT	ATAAAAAAGA	TCTTAAGAGT
99-1 7001-13294	TCCTACCCCT	ATAAAAAAGA	TATTAAAGAGT
	2650	2660	2670
10-1 7001-13350	GGGACCATGG	ATAAACACAA	TATTAGATGA
99-1 7001-13294	AGGTCCTTGG	ATAAATACAA	TACTAGATGA
	2680	2690	2700
10-1 7001-13350	CATTAA AACC	AGTGCAGAGT	CAATAGGGAG
99-1 7001-13294	TATTAA AACC	AGTGCAGAAT	CAATAGGAAG
	2710	2720	2730
10-1 7001-13350	TCTATGTCAG	GAATTAGAAT	TTAGGGGGGA
99-1 7001-13294	TCTATGTCAA	GAAC TAGAAT	TCAGAGGGGA

Figure 53 cont'd

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	2740	2750	2760
00-1 7001-13350	AAGCATAATA	GTTAGTCTGA	TATTAAGGAA
99-1 7001-13294	GAGTATACTA	GTTAGCTTGA	TATTAAGGAA
	2770	2780	2790
00-1 7001-13350	TTTTTGGCTG	TATAATTTAT	ACATGCATGA
99-1 7001-13294	TTTCTGGCTG	TATAACTTGT	ACATGTATGA
	2800	2810	2820
00-1 7001-13350	ATCAAAGCAA	CACCCCCTAG	CAGGGAAGCA
99-1 7001-13294	GTCAAACACG	CACCCATTAG	CTGGGAAGCA
	2830	2840	2850
00-1 7001-13350	GTTATTCAAA	CAACTAAATA	AAACATTAAAC
99-1 7001-13294	ACTGTTCAAG	CAATTGAACA	AAACATTAAAC
	2860	2870	2880
00-1 7001-13350	ATCAGTGCAG	AGATTTTTTG	AAATAAAAAA
99-1 7001-13294	ATCTGTGCAG	AGATTTTTTG	AACTGAAGAA
	2890	2900	2910
00-1 7001-13350	GGAAAATGAA	GTAGTAGATC	TATGGATGAA
99-1 7001-13294	AGAAAATGAT	GTGGTTGACC	TATGGATGAA
	2920	2930	2940
00-1 7001-13350	CATACCAATG	CAGTTTGGAG	GAGGAGATCC
99-1 7001-13294	TATACCAATG	CAGTTTGGAG	GGGGAGATCC
	2950	2960	2970
00-1 7001-13350	AGTAGTCTTC	TATAGATCTT	TCTATAGAAG
99-1 7001-13294	AGTAGTTTTT	TACAGATCTT	TTTACAGAAG
	2980	2990	3000
00-1 7001-13350	GACCCCTGAT	TTTTTAACTG	AAGCAATCAG
99-1 7001-13294	GACTCCCGAT	TTCTTAACTG	AAGCAATCAG
	3010	3020	3030
00-1 7001-13350	TCATGTGGAT	ATTCTGTTAA	GAATATCAGC
99-1 7001-13294	CCATGTGGAT	TTACTGTTAA	AAGTGTCAAA
	3040	3050	3060
00-1 7001-13350	CAACATAAGA	AATGAAGCGA	AAATAAGTTT
99-1 7001-13294	CAATATCAAA	GATGAGACTA	AGATACGATT
	3070	3080	3090
00-1 7001-13350	CTTCAAAGCC	TTACTGTCAA	TAGAAAAAAA
99-1 7001-13294	TTTCAAAGCC	TTATTATCTA	TAGAAAAGAA
	3100	3110	3120
00-1 7001-13350	TGAACGTGCT	ACACTGACAA	CACTAATGAG
99-1 7001-13294	TGAACGTGCT	ACATTAACAA	CACTAATGAG

Figure 53 cont'd

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	3130	3140	3150
00-1 7001-13350	AGATCCTCAA	GCTGTTGGCT	CAGAGCGACA
99-1 7001-13294	AGACCCTCAG	GCAGTAGGAT	CAGAACGACA
	3160	3170	3180
00-1 7001-13350	AGCAAAGTA	ACAAGTGATA	TCAATAGAAC
99-1 7001-13294	AGCTAAGGTA	ACAAGTGATA	TAAATAGAAC
	3190	3200	3210
00-1 7001-13350	AGCAGTTACC	AGCATCTTAA	GTCTTTCTCC
99-1 7001-13294	AGCAGTTACC	AGCATACTGA	GTCTATCTCC
	3220	3230	3240
00-1 7001-13350	AAATCAACTT	TTCAGCGATA	GTGCTATACA
99-1 7001-13294	GAATCAGCTC	TTCTGTGATA	GTGCTATACA
	3250	3260	3270
00-1 7001-13350	CTACAGTAGA	AATGAAGAAG	AGGTCGGAAAT
99-1 7001-13294	TTATAGTAGA	AATGAGGAAG	AAGTTGGGAT
	3280	3290	3300
00-1 7001-13350	CATTGCTGAC	AACATAACAC	CTGTTTATCC
99-1 7001-13294	CATTGCAGAC	AACATAACAC	CTGTCTATCC
	3310	3320	3330
00-1 7001-13350	TCATGGACTG	AGAGTTTGT	ATGAATCATTT
99-1 7001-13294	TCATGGGCTG	AGAGTGCTCT	ATGAATCACT
	3340	3350	3360
00-1 7001-13350	ACCTTTTTCAT	AAAGCTGAAA	AAGTTGTGAA
99-1 7001-13294	ACCTTTTTCAT	AAGGCTGAAA	AGGTTGTCAA
	3370	3380	3390
00-1 7001-13350	TATGATATCA	GGAACGAAAT	CCATAACCAA
99-1 7001-13294	TATGATATCA	GGCACAAAGT	CTATAACTAA
	3400	3410	3420
00-1 7001-13350	CTTATTACAG	AGAACATCTG	CTATTAAATGG
99-1 7001-13294	TCTATTACAG	AGAACATCTG	CTATCAATGG
	3430	3440	3450
00-1 7001-13350	TGAAGATATT	GACAGAGCTG	TATCCATGAT
99-1 7001-13294	TGAAGATATT	GATAGAGCAG	TGTCTATGAT
	3460	3470	3480
00-1 7001-13350	GCTGGAGAAC	CTAGGATTAT	TATCTAGAAAT
99-1 7001-13294	GTTAGAGAAC	TTAGGGTTGT	TATCTAGAAAT
	3490	3500	3510
00-1 7001-13350	ATTGTCAGTA	GTTGTTGATA	GTATAGAAAT
99-1 7001-13294	ATTGTCAGTA	ATAATTAAATA	GTATAGAAAT

Figure 53 cont'd

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00-1 7001-13350	3520 T C C A A C C A A A	3530 T C T A A T G G T A	3540 G G C T G A T A T G
99-1 7001-13294	A C C A A T C A A G	T C C A A T G G C A	G A T T G A T A T G
00-1 7001-13350	3550 T T G T C A G A T A	3560 T C T A G A A C C C	3570 T A A G G G A G A C
99-1 7001-13294	C T G T C A A A T T	T C C A A G A C C T	T G A G A G A A A A
00-1 7001-13350	3580 A T C A T G G A A T	3590 A A T A T G G A A A	3600 T A G T T G G A G T
99-1 7001-13294	A T C A T G G A A C	A A T A T G G A A A	T A G T A G G A G T
00-1 7001-13350	3610 A A C A T C C C C T	3620 A G C A T C A C T A	3630 C A T G C A T G G A
99-1 7001-13294	G A C A T C T C C T	A G T A T T G T G A	C A T G T A T G G A
00-1 7001-13350	3640 T G T C A T A T A T	3650 G C A A C T A G C T	3660 C T C A T T T G A A
99-1 7001-13294	T G T T G T G T A T	G C A A C T A G T T	C T C A T T T A A A
00-1 7001-13350	3670 A G G G A T A A T C	3680 A T T G A A A A G T	3690 T C A G C A C T G A
99-1 7001-13294	A G G A A T A A T T	A T T G A A A A A T	T C A G T A C T G A
00-1 7001-13350	3700 C A G A A C T A C A	3710 A G A G G T C A A A	3720 G A G G T C C A A A
99-1 7001-13294	C A A G A C C A C A	A G A G G T C A G A	G G G G A C C A A A
00-1 7001-13350	3730 G A G C C C T T G G	3740 G T A G G G T C G A	3750 G C A C T C A A G A
99-1 7001-13294	A A G C C C C T G G	G T A G G A T C A A	G C A C T C A A G A
00-1 7001-13350	3760 G A A A A A A T T A	3770 G T T C C T G T T T	3780 A T A A C A G A C A
99-1 7001-13294	G A A A A A A T T G	G T T C C T G T T T	A T A A T A G A C A
00-1 7001-13350	3790 A A T T C T T T C A	3800 A A A C A A C A A A	3810 G A G A A C A G C T
99-1 7001-13294	A A T T C T T T C A	A A A C A A C A A A	A A G A G C A A C T
00-1 7001-13350	3820 A G A A G C A A T T	3830 G G A A A A A T G A	3840 G A T G G G T A T A
99-1 7001-13294	G G A A G C A A T A	G G G A A A A T G A	G G T G G G T G T A
00-1 7001-13350	3850 T A A A G G G A C A	3860 C C A G G T T T A A	3870 G A C G A T T A C T
99-1 7001-13294	C A A A G G A A C T	C C A G G G C T A A	G A A G A T T G C T
00-1 7001-13350	3880 C A A T A A G A T T	3890 T G T C T T G G A A	3900 G T T T A G G C A T
99-1 7001-13294	C A A C A A G A T T	T G C A T A G G A A	G C T T A G G T A T

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00-1 7001-13350	3910 TAGTTACAAA	3920 TGTGTAA AAC	3930 CTTTATTACC
99-1 7001-13294	TAGCTATAAA	TGTGTGAAAC	CTTTATTACC
00-1 7001-13350	3940 TAGGTTTATG	3950 AGTGTAAATT	3960 TCCTACACAG
99-1 7001-13294	AAGATTTCATG	AGTGTAAACT	TCTTACATAG
00-1 7001-13350	3970 GTTATCTGTC	3980 AGTAGTAGAC	3990 CTATGGAATT
99-1 7001-13294	GTTATCTGTT	AGTAGTAGAC	CCATGGAATT
00-1 7001-13350	4000 CCCAGCATCA	4010 GTTCCAGCTT	4020 ATAGAACAAAC
99-1 7001-13294	CCCAGCTTCT	GTTCCAGCTT	ACAGGACAAAC
00-1 7001-13350	4030 AAATTACCAT	4040 TTTGACACTA	4050 GTCCTATTAA
99-1 7001-13294	AAATTACCAT	TTTGACACTA	GTCCAATCAA
00-1 7001-13350	4060 TCAAGCACTA	4070 AGTGAGAGAT	4080 TTGGGAATGA
99-1 7001-13294	CCAAGCATTA	AGTGAGAGGT	TGGGAACGA
00-1 7001-13350	4090 AGATATTAAT	4100 TTGGTCTTCC	4110 AAAATGCAAT
99-1 7001-13294	AGACATTAAT	TTAGTGTTCC	AAAATGCAAT
00-1 7001-13350	4120 CAGCTGTGGA	4130 ATTAGCATAA	4140 TGAGTGTAGT
99-1 7001-13294	CAGCTGCGGA	ATTAGTATAA	TGAGTGTGTG
00-1 7001-13350	4150 AGAACCAATTA	4160 ACTGGTAGGA	4170 GTCCAAAACA
99-1 7001-13294	AGAACAGTTA	ACTGGTAGAA	GCCCAAAAACA
00-1 7001-13350	4180 GTTAGTTTAA	4190 ATACCTCAAT	4200 TAGAAGAAAT
99-1 7001-13294	ATTAGTCCTA	ATCCCTCAAT	TAGAAGAGAT
00-1 7001-13350	4210 AGACATTATG	4220 CCACCACCAG	4230 TGTTTCAAGG
99-1 7001-13294	AGATATTATG	CCTCCTCCTG	TATTTCAAGG
00-1 7001-13350	4240 GAAATTCAAT	4250 TATAAGCTAG	4260 TAGATAAGAT
99-1 7001-13294	AAAATTCAAT	TATAAACTAG	TTGATAAGAT
00-1 7001-13350	4270 AACTTCTGAT	4280 CAACATATCT	4290 TCAGTCCAGA
99-1 7001-13294	AACCTCCGAT	CAACACATCT	TCAGTCCCTGA

Figure 53 cont'd

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	4300	4310	4320
00-1 7001-13350	C A A A T A G A T	A T G T T A A C A C	T G G G G A A A A T
99-1 7001-13294	C A A A T A G A C	A T A T T A A C A C	T A G G G A A A G A T
	4330	4340	4350
00-1 7001-13350	G C T C A T G C C C	A C T A T A A A A G	G T C A G A A A A C
99-1 7001-13294	G C T T A T G C C T	A C C A T A A A A G	G T C A A A A A A C
	4360	4370	4380
00-1 7001-13350	A G A T C A G T T C	C T G A A C A A G A	G A G A G A A T T A
99-1 7001-13294	T G A T C A G T T C	T T A A A T A A G A	G A G A A A A C T A
	4390	4400	4410
00-1 7001-13350	T T T C C A T G G G	A A T A A T C T T A	T T G A G T C T T T
99-1 7001-13294	T T T T C A T G G A	A A T A A T T T A A	T T G A A T C T T T
	4420	4430	4440
00-1 7001-13350	G T C A G C A G C G	T T A G C A T G T C	A T T G G T G T G G
99-1 7001-13294	A T C T G C A G C A	C T T G C A T G C C	A C T G G T G T G G
	4450	4460	4470
00-1 7001-13350	G A T A T T A A C A	G A G C A A T G T A	T A G A A A A T A A
99-1 7001-13294	G A T A T T A A C A	G A A C A G T G C A	T A G A A A A C A A
	4480	4490	4500
00-1 7001-13350	T A T T T T C A A G	A A A G A C T G G G	G T G A C G G G T T
99-1 7001-13294	T A T C T T T A G G	A A A G A T T G G G	G T G A T G G G T T
	4510	4520	4530
00-1 7001-13350	C A T A T C G G A T	C A T G C T T T T A	T G G A C T T C A A
99-1 7001-13294	C A T C T C A G A T	C A T G C C T T C A	T G G A T T T C A A
	4540	4550	4560
00-1 7001-13350	A A T A T T C C T A	T G T G T C T T T A	A A A C T A A A C T
99-1 7001-13294	G G T A T T T C T A	T G T G T A T T T A	A A A C C A A A C T
	4570	4580	4590
00-1 7001-13350	T T T A T G T A G T	T G G G G G T C C C	A A G G G A A A A A
99-1 7001-13294	T T T A T G T A G T	T G G G G A T C T C	A A G G A A A G A A
	4600	4610	4620
00-1 7001-13350	C A T T A A A G A T	G A A G A T A T A G	T A G A T G A A T C
99-1 7001-13294	T G T A A A A G A T	G A A G A T A T A A	T A G A T G A A T C
	4630	4640	4650
00-1 7001-13350	A A T A G A T A A A	C T G T T A A G G A	T T G A T A A T A C
99-1 7001-13294	C A T T G A C A A A	T T A T T A A G A A	T T G A C A A C A C
	4660	4670	4680
00-1 7001-13350	T T T T T G G A G A	A T G T T C A G C A	A G G T T A T G T T
99-1 7001-13294	C T T T T G G A G A	A T G T T C A G C A	A A G T C A T G T T

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	4690	4700	4710
00-1 7001-13350	T G A A T C A A A G	G T T A A G A A A A	G G A T A A T G T T
99-1 7001-13294	T G A A T C A A A A	G T C A A A A A A A	G A A T A A T G T T
	4720	4730	4740
00-1 7001-13350	A T A T G A T G T A	A A A T T T C T A T	C A T T A G T A G G
99-1 7001-13294	A T A T G A T G T G	A A A T T C C T A T	C A T T A G T A G G
	4750	4760	4770
00-1 7001-13350	T T A T A T A G G G	T T T A A G A A T T	G G T T T A T A G A
99-1 7001-13294	T T A T A T A G G A	T T T A A A A A C T	G G T T T A T A G A
	4780	4790	4800
00-1 7001-13350	A C A G T T G A G A	T C A G C T G A G T	T G C A T G A G G T
99-1 7001-13294	A C A G T T A A G A	G T G G T A G A A T	T G C A T G A G G T
	4810	4820	4830
00-1 7001-13350	A C C T T G G A T T	G T C A A T G C C G	A A G G T G A T C T
99-1 7001-13294	A C C T T G G A T T	G T C A A T G C T G	A A G G A G A G T T
	4840	4850	4860
00-1 7001-13350	G G T T G A G A T C	A A G T C A A T T A	A A A T C T A T T T
99-1 7001-13294	A G T T G A A A T T	A A A T C A A T C A	A A A T T T A T C T
	4870	4880	4890
00-1 7001-13350	G C A A C T G A T A	G A G C A A A G T T	T A T T T T T A A G
99-1 7001-13294	G C A G T T A A T A	G A A C A A A G T C	T A T C T T T G A G
	4900	4910	4920
00-1 7001-13350	A A T A A C T G T T	T T G A A C T A T A	C A G A T A T G G C
99-1 7001-13294	A A T A A C T G T A	T T G A A T T A T A	C A G A C A T G G C
	4930	4940	4950
00-1 7001-13350	A C A T G C T C T C	A C A A G A T T A A	T C A G A A A G A A
99-1 7001-13294	A C A T G C T C T T	A C A C G A T T A A	T T A G G A A A A A
	4960	4970	4980
00-1 7001-13350	G T T G A T G T G T	G A T A A T G C A C	T A T T A A C T C C
99-1 7001-13294	A T T G A T G T G T	G A T A A T G C A C	T C T T T A A T C C
	4990	5000	5010
00-1 7001-13350	G A T T C C A T C C	C C A A T G G T T A	A T T T A A C T C A
99-1 7001-13294	A A G T T C A T C A	C C A A T G T T T A	A T C T A A C T C A
	5020	5030	5040
00-1 7001-13350	A G T T A T T G A T	C C T A C A G A A C	A A T T A G C T T A
99-1 7001-13294	G G T T A T T G A T	C C C A C A A C A C	A A C T A G A C T A
	5050	5060	5070
00-1 7001-13350	T T T C C C T A A G	A T A A C A T T T G	A A A G G C T A A A
99-1 7001-13294	T T T T C C T A G G	A T A A T A T T T G	A G A G G T T A A A

Figure 53 cont'd

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00-1 7001-13350	5080 A A A T T A T G A C	5090 A C T A G T T C A A	5100 A T T A T G C T A A
99-1 7001-13294	A A G T T A T G A T	A C C A G T T C A G	A C T A C A A C A A
00-1 7001-13350	5110 A G G A A A G C T A	5120 A C A A G G A A T T	5130 A C A T G A T A C T
99-1 7001-13294	A G G G A A G T T A	A C A A G G A A T T	A C A T G A C A T T
00-1 7001-13350	5140 G T T G C C A T G G	5150 C A A C A T G T T A	5160 A T A G A T A T A A
99-1 7001-13294	A T T A C C A T G G	C A A C A C G T A A	A C A G G T A C A A
00-1 7001-13350	5170 C T T T G T C T T T	5180 A G T T C T A C T G	5190 G A T G T A A A G T
99-1 7001-13294	T T T T G T C T T T	A G T T C T A C A G	G T T G T A A A G T
00-1 7001-13350	5200 T A G T C T A A A A	5210 A C A T G C A T T G	5220 G A A A A C T T A T
99-1 7001-13294	C A G T T T G A A G	A C A T G C A T C G	G G A A A T T G A T
00-1 7001-13350	5230 G A A A G A T C T A	5240 A A C C C T A A A G	5250 T T C T G T A C T T
99-1 7001-13294	A A A G G A T T T A	A A T C C T A A A G	T T C T T T A C T T
00-1 7001-13350	5260 T A T T G G A G A A	5270 G G G G C A G G A A	5280 A T T G G A T G G C
99-1 7001-13294	T A T T G G A G A A	G G A G C A G G T A	A C T G G A T G G C
00-1 7001-13350	5290 C A G A A C A G C A	5300 T G T G A A T A T C	5310 C T G A C A T C A A
99-1 7001-13294	A A G A A C A G C A	T G T G A A T A T C	C T G A T A T A A A
00-1 7001-13350	5320 A T T T G T A T A C	5330 A G A A G T T T A A	5340 A A G A T G A C C T
99-1 7001-13294	A T T T G T A T A T	A G G A G T T T A A	A G G A T G A C C T
00-1 7001-13350	5350 T G A T C A T C A T	5360 T A T C C T T T G G	5370 A A T A C C A G A G
99-1 7001-13294	T G A T C A C C A T	T A C C C A T T A G	A A T A T C A A A G
00-1 7001-13350	5380 A G T T A T A G G A	5390 G A A T T A A G C A	5400 G G A T A A T A G A
99-1 7001-13294	G G T A A T A G G T	G A T C T A A A T A	G G G T G A T A G A
00-1 7001-13350	5410 T A G C G G T G A A	5420 G G G C T T T C A A	5430 T G G A A A C A A C
99-1 7001-13294	T A G T G G T G A A	G G A T T A T C A A	T G G A A A C C A C
00-1 7001-13350	5440 A G A T G C A A C T	5450 C A A A A A A C T C	5460 A T T G G G A T T T
99-1 7001-13294	A G A T G C A A C T	C A A A A A A C T C	A T T G G G A C T T

Figure 53 cont'd

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(Sheet 128 of 132)

00-1 7001-13350	G A T A C A C A G A	5470	G T A A G C A A A G	5480	A T G C T T T A T T	5490
99-1 7001-13294	G A T A C A C A G A		A T A A G T A A A G		A T G C T T T A T T	
00-1 7001-13350	A A T A A C T T T A	5500	T G T G A T G C A G	5510	A A T T T A A G G A	5520
99-1 7001-13294	G A T A A C A T T G		T G T G A T G C A G		A A T T C A A A A A	
00-1 7001-13350	C A G A G A T G A T	5530	T T T T T T A A G A	5540	T G G T A A T T C T	5550
99-1 7001-13294	C A G A G A T G A T		T T C T T T A A G A		T G G T A A T C C T	
00-1 7001-13350	A T G G A G G A A A	5560	C A T G T A T T A T	5570	C A T G C A G A A T	5580
99-1 7001-13294	T T G G A G A A A A		C A T G T A T T A T		C T T G T A G A A T	
00-1 7001-13350	T T G C A C T A C T	5590	T A T G G G A C A G	5600	A C C T C T A T T T	5610
99-1 7001-13294	C T G T A C A G C T		T A T G G A A C A G		A T C T T T A C T T	
00-1 7001-13350	A T T C G C A A A G	5620	T A T C A T G C T A	5630	A A G A C T G C A A	5640
99-1 7001-13294	A T T T G C A A A G		T A T C A T G C G G		T G G A C T G C A A	
00-1 7001-13350	T G T A A A A T T A	5650	C C T T T T T T T G	5660	T G A G A T C A G T	5670
99-1 7001-13294	T A T A A A A T T A		C C A T T T T T T G		T A A G A T C T G T	
00-1 7001-13350	A G C C A C C T T T	5680	A T T A T G C A A G	5690	G T A G T A A A C T	5700
99-1 7001-13294	A G C T A C T T T T		A T T A T G C A A G		G A A G C A A A T T	
00-1 7001-13350	G T C A G G G C T C A	5710	G A A T G C T A C A	5720	T A C T C T T A A C	5730
99-1 7001-13294	A T C A G G G T C A		G A A T G T T A C A		T A C T T T T A A C	
00-1 7001-13350	A C T A G G C C A C	5740	C A C A A C A A T T	5750	T A C C C T G C C A	5760
99-1 7001-13294	A T T A G G T C A T		C A C A A T A A T C		T A C C C T G T C A	
00-1 7001-13350	T G G A G A A A T A	5770	C A A A A T T C T A	5780	A G A T G A A A A T	5790
99-1 7001-13294	T G G A G A A A T A		C A A A A T T C C A		A A A T G A G A A T	
00-1 7001-13350	A G C A G T G T G T	5800	A A T G A T T T T T	5810	A T G C T G C A A A	5820
99-1 7001-13294	A G C A G T G T G T		A A T G A T T T C T		A T G C C T C A A A	
00-1 7001-13350	A A A A C T T G A C	5830	A A T A A A T C T A	5840	T T G A A G C C A A	5850
99-1 7001-13294	G A A A C T G G A C		A A C A A A T C A A		T T G A A G C A A A	

Figure 53 cont'd

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00-1 7001-13350	CTGTA AATCA	CTTTTATCAG	GGCTAAGAAT
99-1 7001-13294	CTGCA AATCT	CTTCTATCAG	GATTGAGAAT
00-1 7001-13350	ACCGATAAAT	AAGAAAGAAT	TAAATAGACA
99-1 7001-13294	ACCTATAAAC	AAAAAGGAGT	TAAATAGACA
00-1 7001-13350	GAGAAAGGTTA	TTAACACTAC	AAAGCAACCA
99-1 7001-13294	AAAGAAATTG	TTAACACTAC	AAAGTAACCA
00-1 7001-13350	TTCTTCTGTA	GCAACAGTTG	GAGGTAGCAA
99-1 7001-13294	TTCTTCTATA	GCAACAGTTG	GCGGCAGTAA
00-1 7001-13350	GGTCATAGAG	TCTAAATGGT	TAAACAACAA
99-1 7001-13294	GATTATAGAA	TCCAATGGT	TAAAGAATAA
00-1 7001-13350	GGCAAACACA	ATAATTGATT	GGTTAGAACAA
99-1 7001-13294	AGCAAAGTACA	ATAATTGATT	GGTTAGAGCAA
00-1 7001-13350	TATTTTAAAT	TCTCCAAAAG	GTGAATTAAA
99-1 7001-13294	TATTTTGAAT	TCTCCAAAAG	GTGAATTAAA
00-1 7001-13350	TTATGATTTT	TTTGAAGCAT	TAGAAAATAC
99-1 7001-13294	CTATGATTTT	TTTGAAGCAT	TAGAGAACAC
00-1 7001-13350	TTACCCTAAT	ATGATTAAAC	TAAATAGATAA
99-1 7001-13294	ATACCCTCAAT	ATGATCAAGC	TTATAGATAA
00-1 7001-13350	TCTAGGGAAT	GCAGAGATAA	AAAAACTGAT
99-1 7001-13294	TTTGGGAAT	GCAGAAATAA	AGAAACTAAT
00-1 7001-13350	CAAAGTAACT	GGATATATGC	TTGTAAGTAA
99-1 7001-13294	CAAGGTCAC	GGGTATATGC	TTGTGAGTAA
00-1 7001-13350	AAAATGAAAA	ATGATAAAAA	TGATAAAATA
99-1 7001-13294	GAAGT - AATA	ATAATGATAA	TGATTAAACCA
00-1 7001-13350	GGTGACAACT	TCATACTATT	CC - AAAGTAA
99-1 7001-13294	- - - TAATC	TCACACAACT	GAGAAAATAA

Figure 53 cont'd

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	6250	6260	6270
0-1 7001-13350	T C A T T T G A T T	A T G C A A T T A T	G T A A T A G T T A
9-1 7001-13294	T C G T C T A A C A	G T T T A G T T G A	T C A T T A G T T A
	6280	6290	6300
0-1 7001-13350	A T T A A A A A C T	A A A A A T C A A A	A G T T A G A A A C
9-1 7001-13294	T T T A A A A T T A	T A A A A T A G T A	A C T A A C T G A T
	6310	6320	6330
0-1 7001-13350	T A A C A A C T G T	C A T T A A G T T T	A T T A A A A A T A
9-1 7001-13294	A A A A A A T C A G	A A A T T G A A A T	T G A A T G T A T A
	6340	6350	6360
0-1 7001-13350	A G A A A T T A T A	A T T G G A T G T A	T A C G
9-1 7001-13294	C G G T T T T T T T	G C C G T	

Figure 53 cont'd

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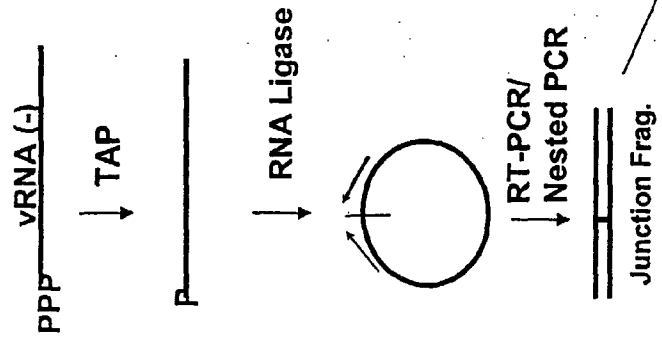
131/132

PCT/US03/05271

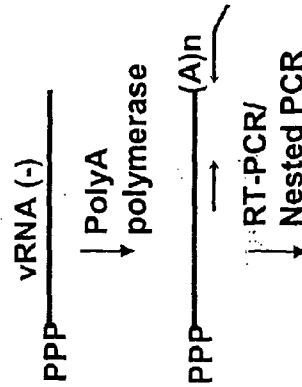
FIGURE 54

APPROACHES

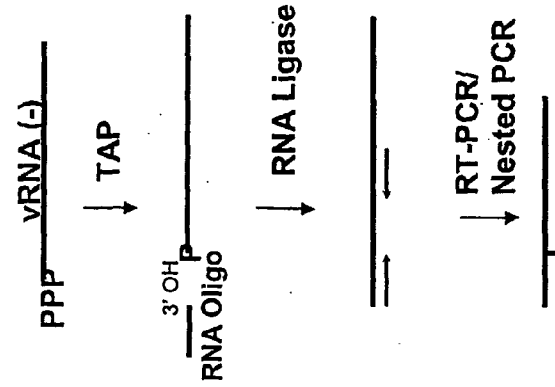
A. Self Ligation



B. 3' RACE

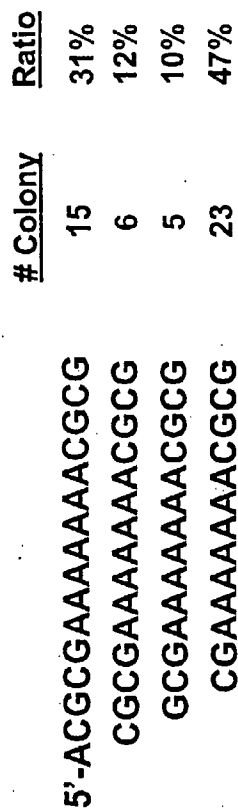


C. 5' RACE



Consensus Sequence Analysis
or Clonal Sequence Analysis

Clonal Analysis of 96 PCR colonies



Total 49 near full-length clones

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PCT/US03/05271

SEQUENCE LISTING

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ViroNovative BV

<120> METAPNEUMOVIRUS STRAINS AND THEIR
USE IN VACCINE FORMULATIONS AND AS
VECTORS FOR EXPRESSION OF
ANTIGENIC SEQUENCES

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<140> To be assigned

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(M) and fusion protein (F) genes

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complete cds

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ggtacttgca acagctgtga atgatctcaa ggactttata agtaaaaaat tgacacctgc 540
aataaacagg aacaagtgtg acatctcaga ccttaagatg gcagtgcgct ttggacaata 600
caatcggagg ttctctcaatg ttgtaagaca gttttctgac aatgcaggta ttacgcctgc 660
aatatctcta gatttaata gaacgcctga gcttgtaaga gctgtaagca acatgccac 720
atcttcaggga cagatcaatc tgatgcttga gaatcgggca atggtcagaa ggaaaggatt 780
tgggattttg attggagttt atggtagctc tgtggtctat atagtgcagc ttctattttt 840
cgggtgtgata gatacacggt gttggaagg gaaggctgct ccattatgtt cagggaaga 900
cgggaattat gcatgtctct tgcgagagg ccaagggttg tattgtcaaa atgctggatc 960
cacagtttat tatccaaatg agggaggactg tgaagtaaga agtgatcatg tgttttgtga 1020
cacagcagct gggataaatg tagcaaaagg gtcagaagag tgcaacagga atatctcaac 1080
aacaagtac ccttgcaagg taagtacagg gcgtcaccca ataagcatgg tggccttacc 1140
accactgggt gctttgtag cctgttatga cgttatgagt tgttcattg gaagcaaca 1200
ggttggaata atcagacctt tggggaagg ttgttcatac atcagcaatc aagatgctga 1260
cactgttaca attgacaaca cagtgtacca attgagcaaa gttgaaggag aacaacacac 1320
aattaaaggg aagccagtat ctacgaattt tgaccctata gagttccctg aagatcagtt 1380
caacgtagcc ctggatcagg tgtttgaaag tgttgagaag agtcagaatc tgatagacca 1440
gtcaacaag atattggata gcattgaaaa ggggaatgca ggatttgtca tagtgatgac 1500
cctcattgtc ctgctcatgc tggcagcagt tgggtgtggg gtcttctttg ttgtaagaa 1560
gagaaaagct gctcccaaat tcccaatgga aatgaatggg gtgaacaaca aaggatttat 1620
cccttaattt tagttattaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1666
```

```
<210> 4
<211> 1636
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (13)...(1629)
<223> Turkey rhinotracheitis virus gene for fusion
protein (F1 and F2 subunits), complete cds
```

```
<400> 4
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agctgcatac aagaaacata caatgaagaa tcttgcagta ctgtaactag aggttataag 120
agtgtgttaa ggacagggtg gtatacgaat gtatttaacc tcgaaatagg gaatgttgag 180
aacatcactt gcaatgatgg acccagccta attgacactg agttagtact cacaagaat 240
gctttgaggg agctcaaaac agtgtcagct gatcaagtgg ctaaggaaaag cagactatcc 300
tcaccaggga gacgtagatt tgtactgggt gcaatagcac ttggtgttgc gacagctgct 360
gccgtaacag ctggtgtagc acttgcaaag acaattagat tagagggaga ggtgaaggca 420
attaagaatg cctccggaa cacaaatgag gcagtatcca cattaggga tgggtgtgag 480
gtactagcaa ctgcagtc aaacaaatga tatagcagat ataaagatgg caattagttt tggccaaaat 540
attaaccaga acaaatgcaa ttagcagatg tctctgata gtgcaggtat cacatcagct 600
aacagaagg tctgaatgt agatgatgaa cttgttagag caattaacag aatgccact 660
tcatcaggac agattagttt gatgttgaa aatcgtgcc tgggttagaag gaaggggttt 720
ggtatattga ttggtgttta tgatggaac gtcgtttata tgggtacaact gcccatattc 780
ggcgtgattg agacacctt ttggagggtg gtggcagcac cactctgtag gaaagagaaa 840
ggcaattatg cttgtatact gagagaagat caagggtgtt actgtacaaa tgcgtgctct 900
acagcttatt atcctaataa agatgattgt gaggtgaagg atgattatgt attttgtgac 960
acagcagctg gcattaatgt ggccctagaa gttgaacagt gcaactataa catatcgact 1020
```

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```

tctaaatacc catgcaaagt cagcacaggt agacacctg tcagtatggt agccttaacc 1140
cccctagggg gtctagtgtc ttgttatgag agtgtaagtt gctccatagg tagcaataaa 1200
gtagggataa taaaacagct aggcaaaggg tgcacccaca ttcccaacaa cgaagctgac 1260
acgataacca ttgataacac tgtgtaccaaa ttgagcaagg ttgtaggcga acagaggacc 1320
ataaaaggag ctccagttgt gaacaatttt aacccaatat tattccctga ggatcagttc 1380
aatgttgacac ttgaccaagt atttgagagt atagatagat ctcaggactt aatagataag 1440
tctaacgact tgctaggtgc agatgccaaag agcaaggctg gaattgctat agcaatagta 1500
gtgctagtca ttctaggaat cttcttttta cttgcagtga tatattactg ttccagagtc 1560
cggaagacca aaccaaagca tgattaccocg gccacgacag gtcatagcag catggcttat 1620
gtcagttaaag ttattt 1636

```

<210> 5

<211> 1860

<212> DNA

<213> pneumovirus

<220>

<221> CDS

<222> (1)...(110)

<223> Avian pneumovirus matrix protein (M) gene, partial
cgs

<220>

<221> CDS

<222> (216)...(1829)

<223> Avian pneumovirus fusion glycoprotein (F) gene,
complete cds

<400> 5

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gagttcaggt aatagtggag ttaggggcat acgttcaagc agaaagcata agcagaatct 60
gcaggaaactg gagccaccag ggtacgagat atgtcctgaa gtcaagataa acacagagag 120
tacacttacc aaatcacagt aacaatttcg tttttaaccc tctcatagtt attacctagc 180
ttgatattat ttagaaaaaa ttgggacaag tgaatgtgc ttggaaaagt gtactgctat 240
tggtatttgt agctacccca acgggggggc tagaagaaag ttatctagag gactcatgca 300
gtactgttac tagaggatac ctgagtggtt tgaggacagg atggtataca aatgtgttca 360
cacttgaggt tggagatgtg gaaaatctca catgtaccga cgggccacgc ttaataagaa 420
cagaacttga actgacaaaa aatgcacttg aggaactcaa gacagtatca gcagatcaat 480
tggcaaagga agctaggata atgtcaccaa gaaaagcccg gtttgttctg ggtgccatag 540
cattaggtgt ggcaactgct gctgctgtga cggctggtgt agcgatagcc aagacaatta 600
ggctagaagg agaagtggct gcaatcaagg gtgcgctcag gaaaacaaat gaggctgtat 660
ctacattagg aaatggcgtg aggggtactt caacagctgt gaatgatctc aaggacttta 720
taagtaaaaa attgacacct gcaataaaca ggaacaagtg tgacatctca gaccttaaga 780
tggcagtgag ctttggacaa tacaatcgga ggttccctcaa tgtggttaaga cagttttctg 840
acaatgcagg tattacgcct gcaatatctc tagatttaat gactgacgct gagcttgtaa 900
gagctgtaag caacatgccc acatcttcag gacagatcaa tctgatgctt gagaatcggg 960
caatggtcag aaggaaagga tttgggattt tgattggagt ttatggtagc tctgtggtct 1020
atatagtgca gcttccctatt ttcggtgtga tagatacacc gtgttggaag gtgaaggctg 1080
ctccattatg ttcagggaaa gacgggaatt atgcatgtct cttgcgagag gaccaagggt 1140
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gaagtgatca tgtgttttgt gacacagcag ctgggataaa tgtagcaaa gactcagaag 1260
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gttggtccat tggaaagcaac aagggttgaa taatcagacc tttggggaaa ggggtgttcat 1440
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agagtcagaa tctgatagac cagtcaaaca agatattgga tagcattgaa aagggaatg 1680
caggatttgt catagtgata gtctcatttg tctgtctcat gctggcagca gttggtgtg 1740
gtgtcttctt tgtggttaag aagagaaaag ctgctcccaa attcccaatg gaaatgaatg 1800
gtgtgaacaa caaaggattt atcccttaat tttagttact aaaaaattgg gacaagtga 1860

```

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<210> 6
<211> 574
<212> PRT
<213> paramyxovirus

<220>
<223> paramyxovirus F protein hRSV B

<400> 6
Met Glu Leu Leu Ile His Arg Leu Ser Ala Ile Phe Leu Thr Leu Ala
1 5 10 15
Ile Asn Ala Leu Tyr Leu Thr Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30
Tyr Gln Ser Thr Cys Ser Ala Val Ser Arg Gly Tyr Phe Ser Ala Leu
35 40 45
Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60
Lys Glu Thr Lys Cys Asn Gly Thr Asp Thr Lys Val Lys Leu Ile Lys
65 70 75 80
Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95
Met Gln Asn Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Ala Pro
100 105 110
Gln Tyr Met Asn Tyr Thr Ile Asn Thr Thr Lys Asn Leu Asn Val Ser
115 120 125
Ile Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140
Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145 150 155 160
Glu Gly Glu Val Asn Lys Ile Lys Asn Ala Leu Leu Ser Thr Asn Lys
165 170 175
Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
180 185 190
Leu Asp Leu Lys Asn Tyr Ile Asn Asn Gln Leu Leu Pro Ile Val Asn
195 200 205
Gln Gln Ser Cys Arg Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220
Gln Lys Asn Ser Arg Leu Leu Glu Ile Asn Arg Glu Phe Ser Val Asn
225 230 235 240
Ala Gly Val Thr Thr Pro Leu Ser Thr Tyr Met Leu Thr Asn Ser Glu
245 250 255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270
Leu Met Ser Ser Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300
Ile Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320
Leu Cys Thr Thr Asn Ile Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350
Pro Gln Ala Asp Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Ser Leu Cys Asn Thr
370 375 380
Asp Ile Phe Asn Ser Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400
Asp Ile Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile

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```
<210> 7
<211> 574
<212> PRT
<213> paramyxovirus

<220>
<223> paramyxovirus F protein hRSV A2
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<400>	7														
Met	Glu	Leu	Leu	Ile	Leu	Lys	Ala	Asn	Ala	Ile	Thr	Thr	Ile	Leu	Thr
1				5					10					15	
Ala	Val	Thr	Phe	Cys	Phe	Ala	Ser	Gly	Gln	Asn	Ile	Thr	Glu	Glu	Phe
			20					25					30		
Tyr	Gln	Ser	Thr	Cys	Ser	Ala	Val	Ser	Lys	Gly	Tyr	Leu	Ser	Ala	Leu
		35					40					45			
Arg	Thr	Gly	Trp	Tyr	Thr	Ser	Val	Ile	Thr	Ile	Glu	Leu	Ser	Asn	Ile
	50					55					60				
Lys	Glu	Asn	Lys	Cys	Asn	Gly	Thr	Asp	Ala	Lys	Val	Lys	Leu	Ile	Lys
65					70					75					80
Gln	Glu	Leu	Asp	Lys	Tyr	Lys	Asn	Ala	Val	Thr	Glu	Leu	Gln	Leu	Leu
				85					90					95	
Met	Gln	Ser	Thr	Pro	Pro	Thr	Asn	Asn	Arg	Ala	Arg	Arg	Glu	Leu	Pro
			100					105					110		
Arg	Phe	Met	Asn	Tyr	Thr	Leu	Asn	Asn	Ala	Lys	Lys	Thr	Asn	Val	Thr
		115					120					125			
Leu	Ser	Lys	Lys	Arg	Lys	Arg	Arg	Phe	Leu	Gly	Phe	Leu	Leu	Gly	Val
	130					135					140				
Gly	Ser	Ala	Ile	Ala	Ser	Gly	Val	Ala	Val	Ser	Lys	Val	Leu	His	Leu
145					150					155					160
Glu	Gly	Glu	Val	Asn	Lys	Ile	Lys	Ser	Ala	Leu	Leu	Ser	Thr	Asn	Lys
				165					170					175	
Ala	Val	Val	Ser	Leu	Ser	Asn	Gly	Val	Ser	Val	Leu	Thr	Ser	Lys	Val
			180					185					190		
Leu	Asp	Leu	Lys	Asn	Tyr	Ile	Asp	Lys	Gln	Leu	Leu	Pro	Ile	Val	Asn
	195						200					205			
Lys	Gln	Ser	Cys	Ser	Ile	Ser	Asn	Ile	Glu	Thr	Val	Ile	Glu	Phe	Gln
	210					215					220				
Gln	Lys	Asn	Asn	Arg	Leu	Glu	Glu	Ile	Thr	Arg	Glu	Phe	Ser	Val	Asn
225					230					235					240
Ala	Gly	Val	Thr	Thr	Pro	Val	Ser	Thr	Tyr	Met	Leu	Thr	Asn	Ser	Glu

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```

                245                250                255
Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
                260                265                270
Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
                275                280                285
Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
                290                295                300
Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305                310                315                320
Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
                325                330                335
Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
                340                345                350
Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
                355                360                365
Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Ile Asn Leu Cys Asn Val
370                375                380
Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385                390                395                400
Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
                405                410                415
Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
                420                425                430
Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Met Asp
                435                440                445
Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450                455                460
Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                470                475                480
Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                490                495
Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500                505                510
Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn Ile Met Ile Thr
515                520                525
Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Ser Leu Ile Ala Val
530                535                540
Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545                550                555                560
Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
                565                570

```

<210> 8

<211> 121

<212> PRT

<213> metapneumovirus

<220>

<223> human metapneumovirus01-71 (partial sequence)

<400> 8

```

Leu Leu Ile Thr Pro Gln His Gly Leu Lys Glu Ser Tyr Leu Glu Glu
 1                5                10                15
Ser Cys Ser Thr Ile Thr Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly
                20                25                30
Trp Tyr Thr Asn Val Phe Thr Leu Glu Val Gly Asp Val Glu Asn Leu
35                40                45

Thr Cys Ala Asp Gly Pro Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr
50                55                60
Lys Ser Ala Leu Arg Glu Leu Arg Thr Val Ser Ala Asp Gln Leu Ala

```


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```

65          70          75          80
Arg Glu Glu Gln Ile Glu Asn Pro Arg Gln Ser Arg Phe Val Leu Gly
          85          90          95
Ala Ile Ala Leu Gly Val Ala Thr Ala Ala Val Thr Ala Gly Val
          100          105          110
Ala Ile Ala Lys Thr Ile Arg Leu Glu
          115          120

```

```

<210> 9
<211> 539
<212> PRT
<213> metapneumovirus

```

```

<220>
<223> Human metapneumovirus isolate 00-1 matrix protein
(M) and fusion protein (F) genes

```

```

<400> 9
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1          5          10          15
His Gly Leu Lys Glu Ser Tyr Leu Glu Ser Cys Ser Thr Ile Thr
 20          25          30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35          40          45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
 50          55          60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65          70          75          80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85          90          95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
 100          105          110
Ala Thr Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
 115          120          125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
 130          135          140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
 145          150          155          160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
 165          170          175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
 180          185          190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
 195          200          205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
 210          215          220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
 225          230          235          240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
 245          250          255
Gly Phe Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
 260          265          270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
 275          280          285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
 290          295          300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
 305          310          315          320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
 325          330          335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile

```

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```

          340          345          350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
          355          360          365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
          370          375          380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385          390          395          400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
          405          410          415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
          420          425          430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
          435          440          445
Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
          450          455          460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465          470          475          480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
          485          490          495
Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
          500          505          510
Ile Ile Lys Lys Thr Lys Arg Pro Thr Gly Ala Pro Pro Glu Leu Ser
          515          520          525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
          530          535

```

<210> 10
 <211> 532
 <212> PRT
 <213> Avian pneumovirus

<220>
 <223> Avian pneumovirus fusion protein gene, partial cds

```

<400> 10
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
  1          5          10          15
Gly Gly Leu Glu Glu Ser Tyr Leu Glu Ser Cys Ser Thr Val Thr
          20          25          30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
          35          40          45
Thr Leu Gly Val Gly Asp Val Lys Asn Leu Thr Cys Thr Asp Gly Pro
          50          55          60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
65          70          75          80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
          85          90          95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
          100          105          110
Ala Thr Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
          115          120          125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
          130          135          140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145          150          155          160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
          165          170          175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
          180          185          190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
          195          200          205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp

```

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```

      210      215      220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
225      230      235      240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
      245      250      255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
      260      265      270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Arg Val Lys Ala
      275      280      285
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
      290      295      300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305      310      315      320
Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
      325      330      335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
      340      345      350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
      355      360      365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370      375      380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385      390      395      400
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
      405      410      415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
      420      425      430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
      435      440      445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
      450      455      460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
465      470      475      480
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
      485      490      495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
      500      505      510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
      515      520      525
Gly Val Asn Asn
530

```

<210> 11
 <211> 537
 <212> PRT
 <213> Avian pneumovirus

<220>
 <223> Avian pneumovirus isolate 1b fusion protein mRNA,
 complete cds

```

<400> 11
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
 1      5      10      15
Gly Gly Leu Glu Ser Tyr Leu Glu Ser Cys Ser Thr Val Thr
      20      25      30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
      50      55      60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
65      70      75      80

```

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```

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
      85                      90                      95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
      100                    105                    110

Ala Thr Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
      115                    120                    125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
      130                    135                    140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
      145                    150                    155
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
      165                    170                    175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
      180                    185                    190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
      195                    200                    205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
      210                    215                    220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
      225                    230                    235
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
      245                    250                    255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
      260                    265                    270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
      275                    280                    285
Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
      290                    295                    300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
      305                    310                    315
Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
      325                    330                    335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
      340                    345                    350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
      355                    360                    365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370                    375                    380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
      385                    390                    395
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
      405                    410                    415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
      420                    425                    430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
      435                    440                    445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
      450                    455                    460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
      465                    470                    475
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
      485                    490                    495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
      500                    505                    510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
      515                    520                    525
Gly Val Asn Asn Lys Gly Phe Ile Pro
      530                    535

```

```

<210> 12
<211> 538

```

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PCT/US03/05271

<212> PRT

<213> Turkey rhinotracheitis virus

<220>

<223> Turkey rhinotracheitis virus gene for fusion
protein (F1 and F2 subunits), complete cds

<400> 12

```

Met Asp Val Arg Ile Cys Leu Leu Leu Phe Leu Ile Ser Asn Pro Ser
 1          5          10          15
Ser Cys Ile Gln Thr Tyr Asn Glu Ser Cys Ser Thr Val Thr
 20          25          30
Arg Gly Tyr Lys Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35          40          45
Asn Leu Glu Ile Gly Asn Val Glu Asn Ile Thr Cys Asn Asp Gly Pro
 50          55          60
Ser Leu Ile Asp Thr Glu Leu Val Leu Thr Lys Asn Ala Leu Arg Glu
 65          70          75          80
Leu Lys Thr Val Ser Ala Asp Gln Val Ala Lys Glu Ser Arg Leu Ser
 85          90          95
Ser Pro Arg Arg Arg Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100          105          110
Ala Thr Ala Ala Val Thr Ala Gly Val Ala Leu Ala Lys Thr Ile
115          120          125
Arg Leu Glu Gly Glu Val Lys Ala Ile Lys Asn Ala Leu Arg Asn Thr
130          135          140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145          150          155          160
Ala Val Asn Asp Leu Lys Glu Phe Ile Ser Lys Lys Leu Thr Pro Ala
165          170          175
Ile Asn Gln Asn Lys Cys Asn Ile Ala Asp Ile Lys Met Ala Ile Ser
180          185          190
Phe Gly Gln Asn Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195          200          205
Asp Ser Ala Gly Ile Thr Ser Ala Val Ser Leu Asp Leu Met Thr Asp
210          215          220
Asp Glu Leu Val Arg Ala Ile Asn Arg Met Pro Thr Ser Ser Gly Gln
225          230          235          240
Ile Ser Leu Met Leu Asn Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245          250          255
Gly Ile Leu Ile Gly Val Tyr Asp Gly Thr Val Val Tyr Met Val Gln
260          265          270
Leu Pro Ile Phe Gly Val Ile Glu Thr Pro Cys Trp Arg Val Val Ala
275          280          285
Ala Pro Leu Cys Arg Lys Glu Lys Gly Asn Tyr Ala Cys Ile Leu Arg
290          295          300
Glu Asp Gln Gly Trp Tyr Cys Thr Asn Ala Gly Ser Thr Ala Tyr Tyr
305          310          315          320
Pro Asn Lys Asp Asp Cys Glu Val Arg Asp Asp Tyr Val Phe Cys Asp
325          330          335
Thr Ala Ala Gly Ile Asn Val Ala Leu Glu Val Glu Gln Cys Asn Tyr
340          345          350
Asn Ile Ser Thr Ser Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355          360          365
Pro Val Ser Met Val Ala Leu Thr Pro Leu Gly Gly Leu Val Ser Cys
370          375          380
Tyr Glu Ser Val Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385          390          395          400
Lys Gln Leu Gly Lys Gly Cys Thr His Ile Pro Asn Asn Glu Ala Asp
405          410          415
Thr Ile Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Val Gly
420          425          430

```

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```

Glu Gln Arg Thr Ile Lys Gly Ala Pro Val Val Asn Asn Phe Asn Pro
      435      440      445
Ile Leu Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
      450      455      460

```

```

Glu Ser Ile Asp Arg Ser Gln Asp Leu Ile Asp Lys Ser Asn Asp Leu
465      470      475      480
Leu Gly Ala Asp Ala Lys Ser Lys Ala Gly Ile Ala Ile Ala Ile Val
      485      490      495
Val Leu Val Ile Leu Gly Ile Phe Phe Leu Leu Ala Val Ile Tyr Tyr
      500      505      510
Cys Ser Arg Val Arg Lys Thr Lys Pro Lys His Asp Tyr Pro Ala Thr
      515      520      525
Thr Gly His Ser Ser Met Ala Tyr Val Ser
      530      535

```

```

<210> 13
<211> 537
<212> PRT
<213> Avian pneumovirus

```

```

<220>
<223> Avian pneumovirus fusion glycoprotein (F) gene,
      complete cds

```

```

<400> 13
Met Ser Trp Lys Val Val Leu Leu Leu Val Leu Leu Ala Thr Pro Thr
1      5      10      15
Gly Gly Leu Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Val Thr
      20      25      30
Arg Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
      50      55      60
Ser Leu Ile Arg Thr Glu Leu Glu Leu Thr Lys Asn Ala Leu Glu Glu
      65      70      75      80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Lys Glu Ala Arg Ile Met
      85      90      95
Ser Pro Arg Lys Ala Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
      100      105      110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
      115      120      125
Arg Leu Glu Gly Glu Val Ala Ala Ile Lys Gly Ala Leu Arg Lys Thr
      130      135      140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
      145      150      155      160
Ala Val Asn Asp Leu Lys Asp Phe Ile Ser Lys Lys Leu Thr Pro Ala
      165      170      175
Ile Asn Arg Asn Lys Cys Asp Ile Ser Asp Leu Lys Met Ala Val Ser
      180      185      190
Phe Gly Gln Tyr Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
      195      200      205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
      210      215      220
Ala Glu Leu Val Arg Ala Val Ser Asn Met Pro Thr Ser Ser Gly Gln
      225      230      235      240
Ile Asn Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
      245      250      255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Val Tyr Ile Val Gln
      260      265      270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Lys Val Lys Ala
      275      280      285

```

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PCT/US03/05271

```

Ala Pro Leu Cys Ser Gly Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
 290                295                300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305                310                315

Pro Asn Glu Glu Asp Cys Glu Val Arg Ser Asp His Val Phe Cys Asp
          325                330                335
Thr Ala Ala Gly Ile Asn Val Ala Lys Glu Ser Glu Glu Cys Asn Arg
          340                345                350
Asn Ile Ser Thr Thr Lys Tyr Pro Cys Lys Val Ser Thr Gly Arg His
          355                360                365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
          370                375                380
Tyr Asp Gly Met Ser Cys Ser Ile Gly Ser Asn Lys Val Gly Ile Ile
385                390                395                400
Arg Pro Leu Gly Lys Gly Cys Ser Tyr Ile Ser Asn Gln Asp Ala Asp
          405                410                415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
          420                425                430
Glu Gln His Thr Ile Lys Gly Lys Pro Val Ser Ser Asn Phe Asp Pro
          435                440                445
Ile Glu Phe Pro Glu Asp Gln Phe Asn Ile Ala Leu Asp Gln Val Phe
          450                455                460
Glu Ser Val Glu Lys Ser Gln Asn Leu Ile Asp Gln Ser Asn Lys Ile
465                470                475                480
Leu Asp Ser Ile Glu Lys Gly Asn Ala Gly Phe Val Ile Val Ile Val
          485                490                495
Leu Ile Val Leu Leu Met Leu Ala Ala Val Gly Val Gly Val Phe Phe
          500                505                510
Val Val Lys Lys Arg Lys Ala Ala Pro Lys Phe Pro Met Glu Met Asn
          515                520                525
Gly Val Asn Asn Lys Gly Phe Ile Pro
          530                535

```

```

<210> 14
<211> 1193
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16)...(1191)
<223> Turkey rhinotracheitis virus (strain CVL14/1)
        attachment protien (G) mRNA, complete cds

```

```

<400> 14
gggacaagta tctctatggg gtccaaacta tatatggctc agggcaccag tgcatatcaa 60
actgcagtgg ggttctggct ggacatcggg aggaggtaca tattggctat agtcctatca 120
gctttcgggc tgacctgcac agtcactatt gcactcactg ttagcgctcat agttgaacag 180
tcagtgttag aggagtgcag aaactacaat ggaggagata gagattgggtg gtcaaccacc 240
caggagcagc caactactgc accaagtgcg actccagcag gaaattatgg aggattacaa 300
acggctcgaa caagaaagtc tgaaagctgt ttgcatgtgc aaatttctta tgggtgatatg 360
tatagccgca gtgatactgt actgggtgggt ttgtattgta tgggcttatt ggttctttgc 420
aaatcaggac caatttgtca gcgagataat caagttgacc caacagccct ctgccattgc 480
agggtagatc ttcaagtgt ggactgctgc aaggtgaaca agattagcac taacagcagc 540
accacctctg agccccagaa gaccaaccgc gcatggccta gccaagacaa cacagactcc 600
gatccaaatc cccaaggcat aaccaccagc acagccactc tgctotcaac aagtctgggc 660
ctcatgctca catcgaagac tgggacacac aaatcagggc ccccccagc cttgccgggg 720
agcaacacca acggaaaaac aaccacagac cgagaaccag ggcccacaaa ccaaccaaat 780
tcaaccacca atgggcaaca caataaacac acccaacgaa tgacaacccc gccaaagtcac 840
gacaacacaa gaaccatcct ccagcacaca acaccctggg aaaagacatt cagtacatac 900
aagcccacac actctccgac caacgaatca gatcaatccc tccccacaa tcaaaacagc 960

```

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```
atcaactgtg aacattttga cccccaaggc aaggaaaaaa tctgctacag agtaggttct 1020
tacaactcca atattacaaa gcaatgcaga attgatgtgc ctttgtgttc cacttatagc 1080
acagtgtgca tgaaaacata ctataccgaa ccattcaact gttggaggcg tatctggcgt 1140
tgcttgtgtg atgacggagt tggctctggtt gagtgggtgtt gcactagtta act 1193
```

```
<210> 15
<211> 1260
<212> DNA
<213> rhinotracheitis virus

<220>
<221> CDS
<222> (16)...(1260)
<223> Turkey rhinotracheitis virus (strain 6574)
        attachment protein (G), complete cds
```

```
<400> 15
gggacaagta tccagatggg gtcagagctc tacatcatag aggggggtgag ctcatctgaa 60
atagtcctca agcaagtcct cagaaggagc caaaaaatac tgtaggact ggtgttatca 120
gccttaggct tgacgctcac tagcactatt gttatatcta tttgtattag tgtagaacag 180
gtcaaattac gacagtgtgt ggacacttat tgggcggaaa atggatcctt acatccagga 240
cagtcaacag aaaatacttc aacaagaggt aagactacaa caaaagacc tagaagatta 300
caggcgactg gagcaggaaa gtttgagagc tgtgggtatg tgcaagttgt tgatgggtgat 360
atgcatgata gcagttatgc tgtactgggt ggtgttgatt gtttgggctt attggctctt 420
tgtgaatcag gaccaatttg tcagggagat acttgggtctg aagacggaaa cttctgccga 480
tgcacttttt cttcccatgg ggtgagttgc tgcaaaaaac ccaaaagcaa ggcaaccact 540
gcccagagga actccaaacc agctaacagc aaatcaactc ctcoggtaca ttcagacagg 600
gccagcaaaag aacataatcc ctcccaggg gagcaacccc gcagggggccc aaccagcagc 660
aagacaacta ttgctagcac cccttcaaca gaggacactg ctaaaccaac gattagcaaa 720
cctaaactca ccatcaggcc ctgcgaaaga ggtccatccg gcagcacaaa agcagcctcc 780
agcaccacca gccacaagac caacaccaga ggcaccagca agacgaccga ccagagaccc 840
cgcaccggac ccaactcccga aaggcccaga caaaccacaa gcacagcaac tccgcccccc 900
acaaccccaa tccacaaggg cggggcccca acccccacaa caacaacaga cctcaaggtc 960
aacccaaggg aaggcagcac aagocaaact gcaatacaga aaaaccacaa cacacaaagt 1020
aatcttggtg actgcacact gtctgatcca gatgagccac aaaggatttg ttaccaggta 1080
ggaacttaca atcctagtca atcgggaacc tgcaacatag aggttcacaa atgttccact 1140
tatgggcatg cttgtatggc tacattatat gacaccccat tcaactgctg gcgcaggacc 1200
aggagatgca tctgtgattc cggaggggag ctgattgagt ggtgctgtac tagtcaataa 1260
```

```
<210> 16
<211> 391
<212> PRT
<213> Turkey rhinotracheitis virus

<220>
<223> Turkey rhinotracheitis virus (strain CVL14/1)
        attachment protien (G) mRNA, complete cds
```

```
<400> 16
Met Gly Ser Lys Leu Tyr Met Ala Gln Gly Thr Ser Ala Tyr Gln Thr
1      5      10      15
Ala Val Gly Phe Trp Leu Asp Ile Gly Arg Arg Tyr Ile Leu Ala Ile
20     25     30
Val Leu Ser Ala Phe Gly Leu Thr Cys Thr Val Thr Ile Ala Leu Thr
35     40     45
Val Ser Val Ile Val Glu Gln Ser Val Leu Glu Glu Cys Arg Asn Tyr
50     55     60
Asn Gly Gly Asp Arg Asp Trp Trp Ser Thr Thr Gln Glu Gln Pro Thr
65     70     75     80
Thr Ala Pro Ser Ala Thr Pro Ala Gly Asn Tyr Gly Gly Leu Gln Thr
85     90     95
Ala Arg Thr Arg Lys Ser Glu Ser Cys Leu His Val Gln Ile Ser Tyr
```


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```

      100      105      110
Gly Asp Met Tyr Ser Arg Ser Asp Thr Val Leu Gly Gly Phe Asp Cys
      115      120      125
Met Gly Leu Leu Val Leu Cys Lys Ser Gly Pro Ile Cys Gln Arg Asp
      130      135      140
Asn Gln Val Asp Pro Thr Ala Leu Cys His Cys Arg Val Asp Leu Ser
145      150      155      160
Ser Val Asp Cys Cys Lys Val Asn Lys Ile Ser Thr Asn Ser Ser Thr
      165      170      175
Thr Ser Glu Pro Gln Lys Thr Asn Pro Ala Trp Pro Ser Gln Asp Asn
      180      185      190
Thr Asp Ser Asp Pro Asn Pro Gln Gly Ile Thr Thr Ser Thr Ala Thr
      195      200      205
Leu Leu Ser Thr Ser Leu Gly Leu Met Leu Thr Ser Lys Thr Gly Thr
      210      215      220
His Lys Ser Gly Pro Pro Gln Ala Leu Pro Gly Ser Asn Thr Asn Gly
225      230      235      240
Lys Thr Thr Thr Asp Arg Glu Pro Gly Pro Thr Asn Gln Pro Asn Ser
      245      250      255
Thr Thr Asn Gly Gln His Asn Lys His Thr Gln Arg Met Thr Pro Pro
      260      265      270
Pro Ser His Asp Asn Thr Arg Thr Ile Leu Gln His Thr Thr Pro Trp
      275      280      285
Glu Lys Thr Phe Ser Thr Tyr Lys Pro Thr His Ser Pro Thr Asn Glu
      290      295      300
Ser Asp Gln Ser Leu Pro Thr Thr Gln Asn Ser Ile Asn Cys Glu His
305      310      315      320
Phe Asp Pro Gln Gly Lys Glu Lys Ile Cys Tyr Arg Val Gly Ser Tyr
      325      330      335
Asn Ser Asn Ile Thr Lys Gln Cys Arg Ile Asp Val Pro Leu Cys Ser
      340      345      350
Thr Tyr Ser Thr Val Cys Met Lys Thr Tyr Tyr Thr Glu Pro Phe Asn
      355      360      365
Cys Trp Arg Arg Ile Trp Arg Cys Leu Cys Asp Asp Gly Val Gly Leu
      370      375      380
Val Glu Trp Cys Cys Thr Ser
385      390

```

<210> 17
 <211> 414
 <212> PRT
 <213> rhinotracheitis virus

<220>
 <223> Turkey rhinotracheitis virus (strain 6574)
 attachment protein (G), complete cds

```

<400> 17
Met Gly Ser Glu Leu Tyr Ile Ile Glu Gly Val Ser Ser Ser Glu Ile
 1      5      10      15
Val Leu Lys Gln Val Leu Arg Arg Ser Gln Lys Ile Leu Leu Gly Leu
      20      25      30
Val Leu Ser Ala Leu Gly Leu Thr Leu Thr Ser Thr Ile Val Ile Ser
      35      40      45
Ile Cys Ile Ser Val Glu Gln Val Lys Leu Arg Gln Cys Val Asp Thr
      50      55      60
Tyr Trp Ala Glu Asn Gly Ser Leu His Pro Gly Gln Ser Thr Glu Asn
      65      70      75      80
Thr Ser Thr Arg Gly Lys Thr Thr Thr Lys Asp Pro Arg Arg Leu Gln
      85      90      95
Ala Thr Gly Ala Gly Lys Phe Glu Ser Cys Gly Tyr Val Gln Val Val
      100      105      110

```

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```

Asp Gly Asp Met His Asp Arg Ser Tyr Ala Val Leu Gly Gly Val Asp
      115      120      125
Cys Leu Gly Leu Leu Ala Leu Cys Glu Ser Gly Pro Ile Cys Gln Gly
      130      135      140

Asp Thr Trp Ser Glu Asp Gly Asn Phe Cys Arg Cys Thr Phe Ser Ser
145      150      155      160
His Gly Val Ser Cys Cys Lys Lys Pro Lys Ser Lys Ala Thr Thr Ala
      165      170      175
Gln Arg Asn Ser Lys Pro Ala Asn Ser Lys Ser Thr Pro Pro Val His
      180      185      190
Ser Asp Arg Ala Ser Lys Glu His Asn Pro Ser Gln Gly Glu Gln Pro
      195      200      205
Arg Arg Gly Pro Thr Ser Ser Lys Thr Thr Ile Ala Ser Thr Pro Ser
      210      215      220
Thr Glu Asp Thr Ala Lys Pro Thr Ile Ser Lys Pro Lys Leu Thr Ile
225      230      235
Arg Pro Ser Gln Arg Gly Pro Ser Gly Ser Thr Lys Ala Ala Ser Ser
      245      250      255
Thr Pro Ser His Lys Thr Asn Thr Arg Gly Thr Ser Lys Thr Thr Asp
      260      265      270
Gln Arg Pro Arg Thr Gly Pro Thr Pro Glu Arg Pro Arg Gln Thr His
      275      280      285
Ser Thr Ala Thr Pro Pro Pro Thr Thr Pro Ile His Lys Gly Arg Ala
      290      295      300
Pro Thr Pro Lys Pro Thr Thr Asp Leu Lys Val Asn Pro Arg Glu Gly
305      310      315
Ser Thr Ser Pro Thr Ala Ile Gln Lys Asn Pro Thr Thr Gln Ser Asn
      325      330      335
Leu Val Asp Cys Thr Leu Ser Asp Pro Asp Glu Pro Gln Arg Ile Cys
      340      345      350
Tyr Gln Val Gly Thr Tyr Asn Pro Ser Gln Ser Gly Thr Cys Asn Ile
      355      360      365
Glu Val Pro Lys Cys Ser Thr Tyr Gly His Ala Cys Met Ala Thr Leu
      370      375      380
Tyr Asp Thr Pro Phe Asn Cys Trp Arg Arg Thr Arg Arg Cys Ile Cys
385      390      395      400
Asp Ser Gly Gly Glu Leu Ile Glu Trp Cys Cys Thr Ser Gln
      405      410

```

```

<210> 18
<211> 13294
<212> DNA
<213> human metapneumo virus

```

```

<220>
<221> misc_feature
<222> (0)...(0)
<223> human MPV protein

```

```

<400> 18
acgcgaaaaa aacgcgtata aattaaattc caaacaaaac gggacaaata aaaatgtctc 60
ttcaagggat tcacctaatg gatctatcat ataaacatgc tatattaaaa gagtctcaat 120
acacaataaa aagagatgta ggcaccacaa ctgcagtgac accttcatca ttacaacaag 180
aaataacact tttgtgtggg gaaatacttt acactaaaca cactgattac aaatatgctg 240
ctgagatagg aatacaatat atttgcacag ctctaggatc agaaagagta caacagattt 300
tgagaaactc aggtagtga gttcaggtgg ttctaaccac aacatactcc ttagggaaag 360
gcaaaaacag taaaggggaa gagctgcaga tgtagatat acatggagtg gaaaagagtt 420
ggatagaaga aatagacaaa gaggcaagaa agacaatggt aactttgctt aaggaatcat 480
caggtaacat ccacaaaaac cagagacctt cagcaccaga cacaccaata atttattat 540
gtgtaggtgc cctaattatc actaaactag catcaacaat agaagttgga ttagagacta 600
cagttagaag agctaataga gtgctaagt atgcactcaa aagataacca aggatagata 660

```

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taccacaaagat	tgctagatct	ttttatgaac	tatttgaaca	aaaagtgtac	tacagaagtt	720
tattcattga	gtacggaaaa	gcttttaggt	catcttcaac	aggaagcaaa	gcagaaaagtt	780
tgtttgaata	tatatattatg	caagccttatg	gagctggcca	aacactgcta	aggtgggggtg	840
tcattgccag	atcatccaac	aacataatgc	tagggcatgt	atctgtgcaa	tctgaattga	900
agcaagttac	agaggtttat	gacttgggtga	gagaaatggg	tcctgaatct	gggcttttac	960
atctaagaca	aagtccaaag	gcagggtgtg	tatcattggc	caattgcccc	aattttgtcta	1020
gtgttgttct	tggcaatgct	tcagggtctag	gcataatcgg	aatgtacaga	gggagagtag	1080
caaacacaga	gctattttct	gcagcagaaa	gttatgccag	aagcttaaaa	gaaagcaata	1140
aaatcaactt	ctcttcgtta	gggcttacag	atgaagaaaa	agaagctgca	gaacacttct	1200
taaacatgag	tggtgacaat	caagatgatt	atgagtaatt	aaaaaactgg	gacaagtcaa	1260
aatgtcattc	cctgaaggaa	aggatattct	gttcattgggt	aatgaagcag	caaaaatagc	1320
cgaagcttct	cagaaatcac	tgaaaaaatc	aggtcacaa	agaactcaat	ctattgttag	1380
ggaaaaagtt	aacactatat	cagaaaactct	agaactacct	accatcagca	aacctgcag	1440
atcatctaca	ctgctggaa	caaaaattggc	atgggcagac	aacagcggaa	tcacccaaat	1500
cacagaaaaa	ccagcaacca	aaacaacaga	tcctgttgaa	gaagaggaat	tcaatgaaaa	1560
gaaagtgtta	ccttccagt	atgggaagac	tcctgcagag	aaaaaatcaa	agttttcaac	1620
cagtgtaaaa	aagaaagttt	ccttttacatc	aaatgaacca	gggaaataca	ccaaactaga	1680
gaaagatgcc	ctagatttgc	totcagacaa	tgaggaagaa	gacgcagaat	cctcaatcct	1740
aacttttgag	gagaaagata	catcatcact	aagcattgaa	gctagactag	aatctataga	1800
agagaagttg	agcatgat	taggactgct	tcgtacactt	aacattgcaa	cagcaggacc	1860
aacagctgca	cgagatggaa	ttagggatgc	aatgattgggt	ataagagaag	agctaataag	1920
agagataatt	aaggaagcca	agggaaaagc	agctgaaatg	atggaagaag	agatgaatca	1980
aagatcaaaa	ataggaatg	gcagtgtaaa	actaaccgag	aaggcaaaa	agctcaacaa	2040
aattgtttgaa	gacgagagca	caagcgggtga	atcagaagaa	gaagaagaac	caaaaagaa	2100
tcaggataac	aatcaaggag	aagatattta	tcagttaatc	atgtagttaa	ataaaaaata	2160
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24

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22

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22

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23

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<220>
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<400> 37
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<400> 38
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<210> 55
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<220>
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<400> 73
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25

<210> 74
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<220>
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<400> 74
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27

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<220>
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<400> 75
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28

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<212> DNA
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<220>
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24

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<220>
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<400> 77
accgatgtg ctcacagaac tg

22

<210> 78
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<220>
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<220> <223> Primer	
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<220> <223> Primer	
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ttgagtattg ccctcaatat ctatctgata ataaactata aaatgcaaaa aaacacatct 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacggtc 240
cccacagaca actcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagatacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca 480
cattctccac caccgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
agcacaagaa agagaccgtc cacagcatca gtccaacctg acatcagcgc aacaaccac 600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaatacaa 660
aggaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata 720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagccaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
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cacccaa 907
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ttgagtattg ccctcaatat ctatctgata ataaactata aaatgcaaaa aaacacatct 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacggtc 240
cccacagaca actcagacac caactcaagc ccacagcatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagatacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggacaag ctctagaaca 480
cattctccac caccgggcaac gacaaggacg gcacgcagga accaccactc tcgcacaag 540
cagcacaaga aagagaccgt ccacagcatc agtccaacct gacatcagcg caacaacca 600
caaaaacgaa gaagcaagtc cagcgagccc acaaacatct gcaagcaca caagaatata 660
aaggaaaagc gtggaggcca acacatcaac aacatacaac caaactagtt acaaaaaaat 720
acaaaataac tctaagataa accatgcaga caccaacaat ggagaagcca aaagacaatt 780
cacaatctcc ccaaaaaggc aacaacacca tattagctct gcccaaatct cctggaaaaa 840
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acacccaa 908
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<213> human metapneumo virus
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ctgagtattg ccctcaatat ctatctgata ataaactata aaatgcaaaa aaacacatct 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacggtc 240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca aactcaccag agacagaacc aacatcaaca 360
ccagacacaa caaaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca 480
cactctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct ccgcacaagc 540
agcacaagaa agagaccgtc cacagcatca gcccaccccg acatcagcgc aacaaccac 600
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aggaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata 720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
acactcgccc atataccaaa aataccacaa ccaccccaag aaaaaaactg ggcaaaaaca 900
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cacccaa

907

<210> 87

<211> 907

<212> DNA

<213> human metapneumo virus

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ttgagtattg ccctcaatat ctatctgac ataaactata aaatgcaaaa aaacacatct 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacgggtc 240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca aactcaccag agacagaacc aacatcaaca 360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaacc caaggataag ctccagaaca 480
cattctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct cgcgacaagc 540
agcacaagaa agagaccgtc cacagcatca gtccaaccgc acatcagcgc aacaaccacc 600
aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacacaa 660
aggaaaagcg tggaggccaa cacatcaaca acatacaacc aaactagtta acaaaaaata 720
caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
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cacccaa
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<210> 88

<211> 907

<212> DNA

<213> human metapneumo virus

<400> 88

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ttgagtattg ccctcaatat ctatctgac ataaactata aaatgcaaaa aaacacatct 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacgggtc 240
cccacagata attcagacac caactcaagc ccacaacatc caactcaaca gtccacagaa 300
ggctccacac tctactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa cagaccgccc gcccttcgtc gacacacaca caacaccacc aagcgcaagc 420
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cattctccac catgggcaac gacaaggacg gcacgcagaa ccaccactct cgcgacaagc 540
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aaaaacgaag aagcaagtcc agcgagccca caaacatctg caagcacaac aagaacacaa 660
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caaaataact ctaagataaa ccatgcagac accaacaatg gagaagtcaa aagacaattc 780
acaatctccc caaaaaggca acaacaccat attagctctg cccaaatctc cctggaaaaa 840
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cacccaa
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<213> human metapneumo virus

<400> 89

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ttgagtattg ccctcaatat ctatctgac ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagggaaac tccaacgggtc 240
ccatagaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
gactccacac tccactctgc agcttcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccacc aagtgcagc 420
aggacaagga caagtccggc agtccacaca aaaaacaatc caagggttag ccccaagaaca 480
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cattcccccac catgggcaat gacaaggacg gtccgcggaa ccaccactct cgcgacaagc 540
agcacaagaa aaagactgtc tacagcatca gtccaaccgc acagcagcgc aacaacccac 600
aaacacgaag aaacaagccc agtgagccca caaacatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
caaaaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc aaaaaagcaa caacaccata ttagctccgc ttaaatctcc ctgaaaaaaa 840
cactcaccca tataccaact ataccacaac catccaaga aaaaaggctg ggcaaaaaca 900
cacccaa 907
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<210> 90
<211> 908
<212> DNA
<213> human metapneumo virus

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<400> 90
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cgtgtggcac gcagcaaatg ctttaaaaaat gcctctttga tcctaataagg aataactaca 120
ttgagtatag cctcaatat ctatctgac ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ttcacacccc atggaatcca gcagggaaac tccaacggtc 240
cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccatc aagtgaagc 420
agaacaaaga caagtccggc agtccacaca aaaaacaatc taaggataag cccagaaca 480
cattcccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct cgcgacaagc 540
agcataagaa aaagaccgtc cacagcatca gtccaacctg acagcagcgc aacaacccac 600
aaacacgaag aagcaagccc agtgagcccg caagcatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
taaaaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc caaaaaggca acaacaccat attagctccg cttaaatctc cctggaaaaa 840
acactcgccc atataccaac tataccacaa ccatccaag gaaaaaagct gggtaaaaa 900
acacccaa 908
```

<210> 91
<211> 908
<212> DNA
<213> human metapneumo virus

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<400> 91
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cgtgtggcac gcagcaaatg ctttaaaaaat gcctctttga tcctaataagg aataactaca 120
ttgagtatag cctcaatat ctatctgac ataaactata caatgcaaga aaacacatcc 180
gaatcagaac atcacaccag ctcacacccc atggaatcca gcagagaaac tccaacggtc 240
cctatggaca actcagacac caatccaggc tcacagtatc caactcaaca gtccacagaa 300
ggctccacac tccactttgc agcctcagca agctcaccag agacagaacc aacatcaaca 360
ccagacacaa caagccgccc gcccttcgtc gacacacaca caacaccatc aagtgaagc 420
agaataagga caagtccggc agtccacaca aaaaacaatc taaggataag cccagaaca 480
cattcccccac catgggcaat gacaaggacg gtccgtggaa ccaccactct cgcgacaagc 540
agcataagaa aaagaccgtc cacagcatca gtccaacctg acagcagcgc aacaacccac 600
aaacacgaag aagcaagccc agtgagcccg caagcatctg caagcacagc aagaccacaa 660
aggaagggca tggaggccag cacatcaaca acatacaacc aaactagtta acaaaaaata 720
taaaaataact ctaagataaa ccatgtagac accaacaatt gagaagccaa aaggcaattc 780
acaatctccc caaaaaggca acaacaccat attagctccg cttaaatctc cctggaaaaa 840
acactcgccc atataccaac tataccacaa ccatccaag gaaaaaagct gggtaaaaa 900
acacccaa 908
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<210> 92
<211> 888
<212> DNA
<213> human metapneumo virus

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<400> 92
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
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cgtgtggcac gtagcaaatg ctttaaaaaat gcttcttttaa tctcatagag aataactaca 120
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gaatcagaac accacaccag ctcaccaccc acagaaccca acaaggaagc ttcaacaatc 240
tccacagaca acccagacat caatccaagc tcacagcatc caactcaaca gtccacagaa 300
aaccacacac tcaaccccgcc agcatcagcg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaacccgct gtccctcgta gacagggtcca cagcacaacc aagtgaagc 420
agaacaaaaga caaacccgac agtccacaca atcaacaacc caaacacagc ttccagtaca 480
caatccccac caggacaac aacgaaggca atccgcagag ccaccacttt cgcagtagc 540
agcacaggaa aaagaccaac cacaacatta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacagggttc agcgaaccca caggcgtctg caagcacaat gcaaaactag 660
cacaccaata atataaaacc aaattagtta acaaaaaatg cgagatagct ctaaagcaaa 720
acatgtagggt accaacaatc aagaaaccaa aagacaactc acaatctccc taaaacagca 780
acgacacccat gtcagctttg ctcaaatctc tctgggagaa acttctaccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaaca gcatccaa 888

```

<210> 93

<211> 888

<212> DNA

<213> human metapneumo virus

<400> 93

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cgtgtggcac gcagcaaatg ctttaaaaaat gcttcttttaa tctcatagag aataactaca 120
ctgagtatag ccctcaatat ctatctgata ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaagaaac ttcaacaatc 240
cccatagaca acccagacat caatccaaac tcacagcatc caacccaaca gtccacagaa 300
agcccccacac tcaaccccgcc agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaacccgct gtccctcgta gacagatcca caacacaacc aagtgaagc 420
agaacaaaaga caaacccaac agtccacaca aaaaacaatc caagtacagt ttccagaaca 480
caatccccac tacgggcaac aacgaaggcg gtccctcagag ccaccgcttt cgcacgagc 540
agcacaagaa aaagaccaac cacaacatca gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacaagttc agcgaaccca caggcatctg caagcacaat gcaaagccag 660
cacaccaaca acataaaacc aaattagtta acaaaaaata cgagatagct ctaaagtaaa 720
acatgtagggt accaacaatc aaggaatcaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gtcagttttg ctcaaatctc cctgggagaa actttcgccc acatactaac 840
aacatcacaa ccatctcaag aaaagaaact gggcaaaaaca gcacccaa 888

```

<210> 94

<211> 888

<212> DNA

<213> human metapneumo virus

<400> 94

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atggagggtga aagtagagaa catccgagca gtagacatgc tcaaagcaag agtcaaaaaat 60
cgtgtggcac gcagcaaatg ctttaaaaaat gcttcttttaa tctcgtagg aataactaca 120
ctgagcatag ccctcaatat ctatctgata gtaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacaccag ctcacacccc acagaatcca acaaaggaac ttcaacaatc 240
cccacagaca acccagacat caatccaaat tcacaacatc caactcaaca gtccacagaa 300
agcccccacac tcaacaccgc agcctcggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaacccgct gtccctcgca gacagatcca caacacaacc aagtgaagc 420
agaacaaaaga caaagctgac agtccacaca aaaaacaacc taagtacagc ctccagaaca 480
caatcaccac cagggcaac aacgaaggcg gtccctcagag acaccgctt ccacacgagc 540
agcacaggaa aaagaccaac cacaacatca gtccagtctg gcagcagcac cacaactcaa 600
aatcatgaag aaacaagttc atcgaaccca caggcatctg caagcacaat gcaagaccag 660
gacaccaaca atacaaaaca aaattagtta acaaaaaata caagatagct ctaaagtaaa 720
acatgtagggt accaacagta aagaaatcaa aagacaactc acaatctccc caaaacagca 780
acaacatcat gtcagcttgc ctcaaatctc cctgggagaa actctcgccc acatactaac 840
aacatcacaa ctatctcaag aaaagaaact gggcaaaaaa acactcaa 888

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<210> 95

<211> 887

<212> DNA

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<213> human metapneumo virus

<400> 95

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cgtgtggcac gcagcaaatg ctttaaaaat gcctctttaa tcctcgtagg aataactaca 120
ctgagtatag ccctcaatat ctatctgacg gtaaaactaca caatacaaaa aaccacatcc 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaaggaaac ttcaacaatc 240
ccacagacaa cccagacatc aatccaaatt cacaacatcc aactcaacag tccacagaaa 300
gccccacact caacaccgca gcctcgggtga gcccatcaga aacagaacca gcacaaacac 360
cagacacaaac aaaccgcctg tcctccgcag acagatccac aacacaacca agtgaaagca 420
gaacaaagac aaagctgaca gtccacacaa aaaacaacct aagtacagcc tccagaacac 480
aatcaccacc acgggcaaca acgaaggcgg tcctcagaga caccgccttc cacacgagca 540
gcacaggaiaa aagaccaacc acaacatcag tccagtctgg cagcagcacc acaactcaaa 600
atcatgaaga aacaagttca tcgaaccacac aggcattctgc aagcacaatg caagaccagg 660
acaccaacaa taaaaacaa aattagttaa caaaaaatac aagatagctc taaagtataa 720
catgtaggta ccaacagtaa agaaatcaaa agacaactca taatctcccc aaaacagcaa 780
caacatcatg tcagcttcgc tcaaattctc ctggggagaa ctctcgccca cataactaaa 840
acatcacaaac tatctcaaga aaagaaactg ggcaaaaaaa cactcaa 887
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<210> 96

<211> 888

<212> DNA

<213> human metapneumo virus

<400> 96

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cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgacg ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcca acaaagaaac ttcaacaatc 240
cctatagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
agcctcacac tcaaccccgcc agcctcgggtg agcccatcag aaacagaacc agcatcaaca 360
ccagacacaa caaacgcctt gtctctcgta gacagatcca caacacaacc aagtgaagc 420
agaacaaaga caaaactgac agtccacaaa aaaaacatcc caagtacagt ctctagaaca 480
caatcctcaa tacgggcaac aacgaaggcg gtctcagag ccaccgcctt tcgcacgagc 540
agcacaggag aaagaccaac tacaacatca gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaacca caggcatctg caagcacaat gcaaaaactag 660
cacaccaaca ttgtaaaacc aaattagtta acaaaaaata tgaaatagct ctaaagtataa 720
acatgtagggt gctaacaatc aagaaatcaa aagacatctc ataattcttc caaaacagca 780
acaacatcat gtcaactttg ctcaaattct cctggggagaa actttcgccc ccatactgac 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaaca gcaccaaa 888
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<210> 97

<211> 888

<212> DNA

<213> human metapneumo virus

<400> 97

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cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccctcaatat ctatctgacg ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaagaaac ttcaacaatc 240
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tcagacacaa caagccgcctt gtcttccgta gacagatcca caacacaacc aagtgaagc 420
agagcaaggga caaaaccgac agtccacaag aaaaacatcc caagtacagt ttctagaaca 480
caatcccccac tacgggcaac aacgaaggcg gtctcagag ccaccgcctt tcgcacgagc 540
agcacaggag agggaccaac cacaacatcg gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacaggttc agcgaacca caggcatctg caagcacaat gcaaaaactag 660
cacaccaaca ttgtaaaacc aaattagtta acaaaaaata tgaaatagtt ctaaagtataa 720
acatgtagggt gctaacaatc aagaaatcaa aagacaactc ataattctcc taaaacagca 780
acaacatcat gtcaactttg ctcaaattct cctggggagaa actttcgccc ccatactgac 840
aacatcacaa tcatctcaag aaaagaaact gggcaaaaaca gcaccaaa 888
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<210> 98
<211> 888
<212> DNA
<213> human metapneumo virus

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<400> 98
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cgtgtggcac gtagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactaca 120
ctgagtatag ctctcaatat ctatctgata ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacaccag ctcaccaccc acagaatcca acaagggaagc ttcaacaatc 240
tccacagaca atccagacat caatccaaac tcacagcatt caactcaaca gtccacagaa 300
aaccacacac taaacccgcg agcatcggtg agctcatcag aaacagaacc agcatcaaca 360
ccagacacaa caaacccgct gtctctcgta gacaggacca cagcacaacc aagtgaagc 420
agaacaaaga caaacccgac agtccacaca agaaacaacc caagcacagc ttccagcaca 480
caatccccac caggggtaac aacgaaggca atcctcagag ccaccgtctt ccgcatgagc 540
agcacaggaa aaagaccagc cacaacatta gtccagtcag acagcagcac cacaacccaa 600
aatcatgaag aaacagggtc agcaaaactca caggcatctg caagcacaat gcaaaaactag 660
cactccaaca atataaaacc aaattagtta acaaaaaata cgagatagct cttaaagtaaa 720
acatgtaggc accaacaatc aggaatttaa aagacaactc acaacctccc taaaacagca 780
acgacaccat gtcaactttg ctcaaatctc tctgggagaa actttttgcc acatactaac 840
aacatcacia tcattctcaag aaaagaaact gggcaaaaaca gcatccaa 888
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<210> 99
<211> 888
<212> DNA
<213> human metapneumo virus

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<400> 99
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cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccttcaacat ctatctgata ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
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tcagacacaa caaacccgct gtctctcgta gacagatcca caacacaacc aagtgaagc 420
agagcaagaa caaacccgac agtccacaag aaaaacatcc caagtacagt ttctagaaca 480
caatccccac tacgggcaac aacgaaggcg gtccctcagag ccaccgcctt tcgcatgagc 540
agcacaggag agggaccaac cacaacatcg gtccagtctg acagcagcac cacaacccaa 600
aatcatgaag aaacagggtc agcgaaccca caggcatctg caagcacaat gcaaaaaccag 660
cacaccaaca ttgcaaaaacc aaattagtta acaaaaaata tgaaatagtt cttaaagtaaa 720
acatgtaggc gccacaatc aagaaatcaa aagacaactc acaatctccc taaaacagca 780
acaacatcat gccaaacttg ctcaaatctc cctgggagaa accctcgccc ccatactgac 840
aacatcacia tcattctcaag aaaagaaact gggcaaaaaca gcacaaa 888
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<210> 100
<211> 888
<212> DNA
<213> human metapneumo virus

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<400> 100
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cgtgtggcac gcagcaaatg ctttaaaaat gcttctttaa tcctcatagg aataactact 120
ctgagtatag ccttcaatat ctatctgata ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacactag ctcaccaccc acagaatcta acaaggaaac ttcaacaatc 240
cctatagaca accagacat caatccaaac tcacagcatt caactcaaca gtccacagaa 300
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ccaggcataa caaacccgct gtcttttcta gacagatcca caacacaacc aagtgaagc 420
agaacaaaaga caaacccgac agtccacaaa aaaaacatct caagtacagt ttctagaaca 480
cagtccccac cagggacaac agcgaaggcg gtccccagag ccaccgcctt tcgacagagc 540
agcacaggag aaagaccaac cacaacacca gtccagcccg atagcagcac cacaacacaa 600
aatcatgaag aaacagggtc agcgaaccca caggcatccg caagcacaat gcaaaaaccag 660
cacaccaaca ttgcaagacc aaattagtta acaaaaaata tgaaatagct cttaaagtaaa 720
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acatgtaggt	gccaacaatc	aagaaatcaa	aagataactc	ataatctctc	taaaacatca	780
acaacatcat	gttaactttg	ctcaaattctc	tctgggagaa	accttcgccc	ccatactggc	840
aacatcacaa	tcattctcaag	aaaagaaact	gggcaaaaaca	acacccaaa		888

<210> 101
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 101						
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ctgagttag	ccctcaatat	ctattctgac	ataaactaca	caatacaaaa	aaccacatct	180
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cacaccaaca	ttgcaagacc	aaattagtta	acaaaaaata	tgaaatagct	ctaaagtaaa	720
acatgtaggt	gccaacaatc	aagaaatcaa	aagataactc	ataatctctc	taaaacatca	780
acaacatcat	gttaactttg	ctcaaattctc	tctgggagaa	accttcgccc	ccatactggc	840
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<210> 102
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 102						
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ctgagttag	ccctcaatat	ctattctgac	ataaactaca	caatacaaaa	aaccacatct	180
gaatcagaac	accacactag	ctcaccaccc	acagaatcta	acaaggaaac	ttcaacaatc	240
cctatagaca	accagacat	caatccaaac	tcacagcatc	caactcaaca	gtccacagaa	300
agcctcacac	tctaccccac	atcctcgggtg	agctcatcag	aaacagaacc	agcatcaaca	360
ccaggcataa	caaaccacct	gtcctttgta	gacagatcca	caacacaacc	aagtgaagc	420
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cagtccccac	cacggacaac	agcgaaggcg	gtccccagag	ccaccgccct	tcgcacgagc	540
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aatcatgaag	aaacaggctc	agcgaaccca	caggcatccg	caagcacaat	gcaaaaccag	660
cacaccaaca	ttgcaagacc	aaattagtta	acaaaaaata	tgaaatagct	ctaaagtaaa	720
acatgtaggt	gccaacaatc	aagaaatcaa	aagataactc	ataatctctc	taaaacatca	780
acaacatcat	gttaactttg	ctcaaattctc	tctgggagaa	accttcgccc	ccatactggc	840
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<210> 103
<211> 888
<212> DNA
<213> human metapneumo virus

<400> 103						
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ctgagcatag	ccctcaatat	ctattctgac	ataaactaca	caatacaaca	aaccacatct	180
gaatcagaac	accacaccag	ctcaccaccc	acagaatcca	acaaggaaac	ttcaacaatc	240
tccacagaca	accagacat	caatccaaac	tcacagcatc	caactcaaca	gtccacagaa	300
aacccacac	tcaacccagc	agcatcagcg	agcccatcag	aaacagaatc	agcatcaaca	360
ccagatacaa	caaaccgcct	gtcctcggta	gacaggacca	cggatcaacc	aagtgaagc	420
agaacaaaaga	caaaactgac	agtccacaca	agaaacaacc	taagcacagc	ctccagtaca	480

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caatccccac caggggcaac aacgaaggca atccgcagag ccaccaccct ccgcatgagc 540
agcacaggaa gaagaccaac cacaacacta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca atataaaaacc aaattagtta acaaaaaata cgagatagct ctaaagttaa 720
acatgtaggc accaacaatc aagaaaccaa aagataactc acaatcccc caaaacagca 780
acgacaccat gtcagctttg ctcaaacttc tctgggagaa acttttgccc acatactaac 840
aacatcacia ccattctcaag aaaagaaact gggcaaaaca gcatccaa 888

```

<210> 104
 <211> 888
 <212> DNA
 <213> human metapneumo virus

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<400> 104
atggaggtga aagtagagaa cattcgagca atagacatgc tcaaagcaag agtgaaaaat 60
cgtgtggcac gtagcaaatg ttttaaaaat gtttctttta tctcataggt aataactaca 120
ctgagcatag ccttcaatat ctatctgata ataaactaca caatacaaaa aaccacatct 180
gaatcagaac accacaccag ctccaccacc acagaatcca acaagggaag ttcaacaatc 240
tccacagaca acccagacat caatccaaac tcacagcatc caactcaaca gtccacagaa 300
aaccacacac tcaaccacgc agcatcagcg agcccatcag aaacagaatc agcatcaaca 360
ccagatacaa caaaccgcct gtctctcgta gacaggtcca cggtagaacc aagtgtaaaac 420
agaacaaaaga caaaactgac agtccacaca agaaacaacc taagcacagc ctccagtaca 480
caatccccac caggggcaac aacgaaggca atccgcagag ccaccaccct ccgcatgagc 540
agcacaggaa gaagaccaac cacaacacta gtccagtccg acagcagcac cacaacccaa 600
aatcatgaag aaacaggctc agcgaaccca caggcatctg caagcacaat gcaaaaccag 660
cacaccaaca atataaaaacc aaattagtta acaaaaaata cgagatagct ctaaagttaa 720
acatgtaggc accaacaatc aagaaaccaa aagataactc acaatcccc caaaacagca 780
acgacaccat gtcagctttg ctcaaacttc tctgggagaa acttttgccc acatactaac 840
aacatcacia ccattctcaag aaaagaaact gggcaaaaca gcatccaa 888

```

<210> 105
 <211> 901
 <212> DNA
 <213> human metapneumo virus

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<400> 105
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tctttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgata atcgatcatg caacattaag aaacatgac 180
aaaacagaaa actgtgctaa catgccgtcg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacagag 300
aactcaacat ccccgtagc aaccacagag ggccatccat acacaggagc aactcaaaac 360
tcagacacaa cagctcccca gcaaaccaca gacaaacaca cagcaccgct aaaaatcaacc 420
aatgaacaga tcaccagac aaccacagag aaaaagacaa tcagagcaac aacccaaaa 480
agggaaaaag gaaaagaaaa cacaacccaa accacaagca cagctgcaac ccaaacacac 540
aacaccacca accaaatcag aaatgcaagt gagacaatca caacatccga cagaccacga 600
actgacacca caaccacaaag cagcgaacag acaaccggg caacagacc aagctcccca 660
ccacaccatg catagagagg tgcaaaactc aaatgagcac aacacacaaa catcccatcc 720
aagtagttaa caaaaaacca caaaataacc ttgaaaacca aaaaaccaa acataaaccc 780
agaccagaaa aaacatagac accatatgga aggttctagc atatgcacca atgagatggc 840
atctgttcat gtatcaatag caccaccatc attcaaggaa taagaagagg cgaaaattta 900
a 901

```

<210> 106
 <211> 901
 <212> DNA
 <213> human metapneumo virus

```

<400> 106
atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaagaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tctttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgata attgatcatg caacattaag aaacatgac 180

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aaaacagaaa actgtgctaa catgccatcg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaagcac cgaacccaat ccacagcaag caacacaatg gaccacagag 300
aactcaacat ccccagcagc aaccctagag agccatccat acacagggac aacccaaaca 360
ccagacataa cagctcccca acaaaccaca gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tccccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaaa 480
agggaaaaag aaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaaccag aaatgcaagt gagacaatca caacatccga cagaccaga 600
attgacacca caacccaaag cagcgatcag acaacccggg caacagaccc aagctcccca 660
ccacaccatg cacagagtgg tgcaaaaccc aaatgaacac aacacacaaa catctcatcc 720
aagtagttaa caaaaaacca caaataaacc ttgaaaacca aaaaacccaa ccacaaactt 780
agaccagaa aaacatagac actatatgga aggtttgagc atatgcacca atgaaatggt 840
atctgttcat gtatcaatag cgccaccatt atttaaggaa taagaagagg caaaaattca 900
a

```

<210> 107

<211> 860

<212> DNA

<213> human metapneumo virus

<400> 107

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atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgac atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccgccc gcagaaccaa gcaaaaagac cccaatgacc 240
tctacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat tcccagcagc aacctcagag ggccatctac acacagggac aactcaaaaca 360
ccagacacaa cagctcctca gcaaacacaa gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaaa tccccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag ggaaagaaaa cacaaaccaa accacaagca cagctgctac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
ccacatcatg cacagggaaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gaccagaaa aacatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tttgttcatt tatcaatagc gccaccatta tttaaggaa 840
aagaagaggg aaaaattcaa

```

<210> 108

<211> 861

<212> DNA

<213> human metapneumo virus

<400> 108

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atggaagtaa gagtggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgac atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccgccc gcagaaccaa gcagaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacggag 300
aactcaacat ccccagcagc aacccacagag ggccatctac acacagggac aactcaaaaca 360
ccagacacaa cagctcctca gcaaacacaa gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tccccagggc aaccacagag aaaaagacaa ccagagaaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaacaacc 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccagg caacagaccc aagctcccca 660
gcacaccatg cacagggaaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaaatc agaccagaa aacacagac actatatgga aggtccgagc 780
atatgcaccg atgaaatggc atctgttcat gtatcaatag caccaccatt atttaaggaa 840
taagaagagg caaaaattca a

```

<210> 109

<211> 860

<212> DNA

<213> human metapneumo virus

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<400> 109
atggaagtaa gaggaggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacattga tccttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgac atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgccaccg gcagaacca gcaaaaagac cccaatgacc 240
tccacagcag gcctaaacac taaacccaat ccacagcaag caacacagt gaccacggag 300
aactcaacat cccagcagc aaccccagag ggccatctac acacaggag aactcaaaaca 360
ccagacacaa cagctcctca gcaaacacac gacaaagcaca cagcactgcc aaaatcaacc 420
aatgaacaga tccccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaacccaa accacaagca cagctgcaac ccaaacacac 540
aacaccacca accaaatcag aaatgcaagc gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccc 660
ccacaccatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gaccagaaa aacatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcacg tatcaatagc gccaccatta ttttaaggaa 840
agaagaggc aaaaattcaa 860
```

```
<210> 110
<211> 860
<212> DNA
<213> human metapneumo virus
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```
<400> 110
atggaagtaa gaggaggagaa cattcgagcg atagacatgt tcaaagcaaa gataaaaaaac 60
cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgac atcgatcatg caacattaag aaacatgatc 180
aaaacagaaa attgtgctaa catgcccgcg gcagaacca gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagt gaccacggag 300
aactcaacat cccagcagc aaccccagag ggccatctac acacaggag aactcaaaaca 360
ccagacacaa cagctcctca gcaaacacac gacaaacaca cagcactgcc aaaatcaacc 420
aatgaacaga tccccagac aaccacagag aaaaagacaa ccagagcaac aacccaaaga 480
agggaaaaag gaaaagaaaa cacaacccaa accacaagca cagctgcaac ccaaacacac 540
aacaccacca accaaatcag aaatgcaatt gagacaatca caacatccga cagaccaga 600
actgactcca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccc 660
ccacaccatg cacagggaag tgcaaaaccc aaatgaacac aacacacaaa catcccatcc 720
aagtagttaa caaaaaatca gaccagaaa aacatagaca ctatatggaa ggtccgagca 780
tatgcaccga tgaaatggca tctgttcacg tatcaatagc gccaccatta ttttaaggaa 840
agaagaggc aagaattcaa 860
```

```
<210> 111
<211> 886
<212> DNA
<213> human metapneumo virus
```

```
<400> 111
atggaagtaa gaggaggagaa cattcgggca atagacatgt tcaaagcaaa aatgaaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttatttg attaacagca 120
ttaagtatgg cacttaatat ttttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggaa actgtgttaa tatgcgcgag gtagaaccac gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt ggccgcagag 300
gattcaacat ctctagcagc aacctcagag gaccatctac acacaggag aactcaaaaca 360
ccagatgcaa cagctctctca gcaaacacac gacgagtaca caacattgct gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa ccgagcaac aacccaaaaa 480
gaaaccacaa ctcgaaactc aagcacagct gcaacccaaa cactcaaac taccaacca 540
actagctatg tgagagaggc aaccacaaca tccgccagat ccagaaacag tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaaccaca ccatacacag 660
aaaagcaca caacaacata caacacagac acatcctctc caagtagtta acaaaaaaac 720
tataaataa tcatgaaaac cgaaaacta gaaaagttaa tttgaactca gaaaagaaca 780
caaacactat atgaattggt tgagcgtata tactaatgaa atagcatctg tttgtgcac 840
aataatacca tcattattta agaaataaga agaagctaaa attcaa 886
```

```
<210> 112
```

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<211> 889
 <212> DNA
 <213> human metapneumo virus

```

<400> 112
atggaagtaa gagtggagaa cattcggaca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gcagcaagtg ctatagaaat gctacactga tccttatttg actgacagca 120
ttaagtatgg cacttaatat tttcttgatc atcgattatg caacatttaa aaacatgacc 180
aaagtggaa actgtgctaa tatgccgcg gtagaaccga gtaagaagac cccaatgacc 240
tctacagtag actcaagcac cggacccaat ccacagcaga caacacagtg gaccacagag 300
gattcaacat ctctagcagc aacctcagag gaccatctac acacaggagc aactccaaca 360
ctagatgcaa cagtttctca gcaaaccaca gacaagcaca caacaccgct gagatcaacc 420
aatggacaga ccaccagac aaccacagag aaaaagccaa ccagagcaat agccaaaaaa 480
gaaaccacaa accaaaccac aagcacagct gcaaccacaa cattcaacac caccaatcaa 540
accagaaatg gaagagagac aaccataaca tctgccagat ccagaaacga cgccacaact 600
caaagcagcg aacaaacaaa ccagacaaca gacccaagct cccaaccaca tcatgcatag 660
ataagcacia taacaatatg aacacaacac agacacatct tctccaagta gttaacaaaa 720
aactataaaa taacctatgaa aacaaaaaaa ctagaaaagt aaatttgaac tcagaaaaga 780
acacaaacac taaatgaatt gtttgagcat atatacta atgaaatagcat ctgttcatgc 840
atcaataata ccatcattac ttaagaaata agaagaagca aaaattcaa 889

```

<210> 113
 <211> 885
 <212> DNA
 <213> human metapneumo virus

```

<400> 113
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttatttg attaacagca 120
ttaagtatgg cacttaatat ttttttaatc attgattatg caatgttaaa aaacatgacc 180
aaagtggaa actgtgttaa tatgccgcg gtagaaccac gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaactcaat ccacagcagg caacacagtt gaccacagag 300
gattcaacat ctctagcagc aacctcggag gatcatttac tcacaggagc aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccaccacaa aaccacagag aaaaagccaa ccggagcaac aacaaaaaaa 480
gaaaccacaa ctgcaaccac aagcacagct gcaaccacaa cactcaacac caccaaccaa 540
actagcaatg gaagagaggc aaccacaaca tccaccagat ccagaaacgg tgccacaact 600
aaaaacagcg atcaaaacac ctgacagaca gacccaagct cccaaccaca ccatacacag 660
aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta acaaaaaact 720
ataaaataac catgaaaact aaaaaactag aaaagttaat ttgaactcag aaaagaacac 780
aaacactata tgaattgttt gagcgtatat actaatgaaa tagcatctgt ttgtgcatca 840
ataataccat cattatttaa gaaataagaa gaagctaaaa ttcaa 885

```

<210> 114
 <211> 885
 <212> DNA
 <213> human metapneumo virus

```

<400> 114
atggaagtaa gagtggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgcataagaa gtagcaagtg ctatagaaat gctacactga tccttatttg attaacagca 120
ttaagtatgg cacttaatat ttttttaatc attgattatg caacattaaa aaacatgacc 180
aaagtggaa actgtgttaa tatgccgcg gtagaaccac gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaactcaat ccacagcagg caacacagtt gaccacagag 300
gattcaacat ctctagcagc aacctcagag ggccatccac acacaggaac aactccaaca 360
ccagacgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccaccacaa agccacagag aaaaagccaa ctggagcaac aacaaaaaaa 480
gaaaccacaa cccgaactac aagtacagct gcaaccacaa caccacacac caccaaccaa 540
accagcaatg gaagagaggc aaccacaaca tccgccaggc ccagaaacgg tgccacaact 600
caaaacagcg atcaaaataac ccaggcagca gactcaagct cccaaccaca ccatacacag 660
aaaagcacaa caacagcata caacacagac acatcttttc caagtagtta acaaaaaact 720
ataaaataac catgaaaacc aaaaaactag aaaagttaat ttgaactcag aaaagaacac 780

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aaacactata	tgaattgttt	gagcgtatat	actaatgaaa	tagcatctgt	ttgtgcatca	840
ataataccat	cattatttta	gaaataagaa	gaagctaaaa	ttcaa		885

<210> 115
<211> 886
<212> DNA
<213> human metapneumo virus

<400> 115						
atggaagtaa	gagtggagaa	cattcgggca	atagacatgt	tcaaagcaaa	gatgaaaaac	60
cgtataagaa	gtagcaagt	ctatagaaat	gctacactga	tccttatttg	attaacagca	120
ctaagtatgg	cacttaatat	ttttttaatc	attgattatg	caacattaaa	aaacatgacc	180
aaagtggaa	actgtgttaa	tatgccgccc	gtagaaccaa	gcaagaagac	cccaatgacc	240
tctgcagtag	actcaaacac	caaaccat	ccacagcagg	caacacagtt	gaccacagag	300
gattctacat	ctttagcagc	aaccctagag	gaccatccac	acacagggac	aactccaaca	360
ccagatgcaa	cagtctctca	gcaaaccaca	gacgagcaca	caacactgct	gagatcaacc	420
aacagacaga	ccacccaaac	aactgcagag	aaaaagccaa	ccagggcaac	aacccaaaaa	480
gaaaccacaa	ctcgaaccac	aagcacagct	gcaacccaaa	cactcaacac	caccaaccaa	540
actagcaatg	gaagagaggc	aaccacaaca	tctgccagat	ccagaaacaa	tgccacaact	600
caaagcagcg	atcaaacac	ccaggcagca	gaaccaagct	cccaatcaca	acatacacag	660
aaaagcacia	caacaacata	caacacagac	acatcttctc	taagtagtta	acaaaaaac	720
tataaaataa	ccatgaaaac	caaaaaacta	gaaaagttaa	tttgaactca	gaaaagaaca	780
caaacactat	atgaattatt	tgagcgtata	tactaatgaa	atagcatctg	tttgtgcatc	840
aataatacca	tcattattta	agaaataaga	agaagctaaa	attcaa		886

<210> 116
<211> 887
<212> DNA
<213> human metapneumo virus

<400> 116						
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ctaagtatgg	cacttaatat	ttttttaatc	attgattatg	caaaatcaaa	aaacatgacc	180
agagtggaa	actgtgtcaa	tatgccgccc	gtagaaccaa	gcaagaagac	cccaatgacc	240
tctgcagtag	acttaaacac	caaaccat	ccacagcagg	caacacagtt	gaccacagag	300
gattcaacat	ctctagcagc	aaocctagag	ggccatctac	acacagggac	aactccaaca	360
ccagatgtaa	cagtctctca	gcaaaccaca	gacgagcaca	caacactgct	gagatcaacc	420
aacagacaga	ccacccaaac	agccgcagag	aaaaagccaa	ccagagtaac	aactaacaac	480
gaaaccataa	ctcgaaccac	aagcacagct	gcaacccaaa	cactcaacac	caccaaccaa	540
accaacaatg	gaagagaggc	aaccacaaca	tctgccagat	ccagaaacaa	tgccacaact	600
caaagcagcg	accaaacaac	ccaggcagca	gacccaagct	cccaatcaca	acatacacag	660
aaaagcataa	caacaacata	caacacagac	acatcttctc	caagtagtta	acaaaaaac	720
tataaaataa	ccatgaaaac	caaaaaacta	agaaaagtta	atttgaactc	agaaaagaac	780
acaaacacta	tatgaattgt	ttgagcgtat	ataactaatga	aatagcatct	gtttgtgcat	840
caataatacc	atcattattt	aagaattaag	aagaagctaa	aattcaa		887

<210> 117
<211> 887
<212> DNA
<213> human metapneumo virus

<400> 117						
atggaagtaa	gagtggagaa	cattcgggca	atagacatgt	tcaaagcaaa	gatgaaaaac	60
cgtataagaa	gtagcaagt	ctatagaaat	gctacactga	tccttatttg	attatcagca	120
ctaagtatgg	cacttaatat	ttttttaatc	attgattatg	caaaatcaaa	aacctgacc	180
agagtggaa	actgtgttaa	tatgccgccc	gtagaaccaa	gcaagaagac	cccaatgacc	240
tctgcagtag	acttaaacac	caaaccat	ccacagcagg	caacacagtt	gaccacagag	300
gattcaacat	ctccagcagc	aaccctagag	ggccatctac	acacagggac	aactccaaca	360
ccagatgcaa	cagtctctca	gcaaaccaca	gacgagcaca	caacactgct	gagatcaacc	420
aacagacaga	ccacccaaac	aaccgcagag	aaaaagccaa	ccagagcaac	aacccaaaaa	480
gaaaccataa	ctcgaaccac	aagcacagct	gcaacccaaa	cactcaacac	caccaaccaa	540

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accagcaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaatcaca acatacaaaag 660
aaaagcacaa caacaacata caacacagac acatcttctc caagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaaact agaaaagtta atttgaactc agaaaagaac 780
acaacacta tatgaattgt ttgagcgtat atactaatga aatagcatct gtttgtgcat 840
caataatacc atcattatatt aagaattaag aagaagctaa aattcaa 887
```

<210> 118
<211> 886
<212> DNA
<213> human metapneumo virus

```
<400> 118
atggaagtaa gaggaggagaa cattcgggca atagacatgt tcaaagcaaa gatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttatttgg attaacagca 120
ctaagtatgg cacttaatat ttttttaatc attgattatg caacattaaa aaacatgacc 180
aaagtggaaac actgtgttaa tatgccgccg gtagaaccaa gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt gaccacagag 300
gactctacat ctttagcagc aaccctagag gaccatccac acacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagcaca caacactgct gagatcaacc 420
aacagacaga ccacccaaac aactgcagag aaaaagccaa ccagagcaac aaccaaaaaa 480
gaaaccacaa ctggaaccac aagcacagct gcaacccaaa cactcaacac caccaacca 540
actagcaatg gaagagaggc aaccacaaca tctgccagat ccagaaacaa tgccacaact 600
caaagcagcg atcaacaac ccaagcagca gaaccaaact cccaatcaca acatacacag 660
aaaagcacaa caacaacata caacacagac acatcttctc taagtagtta acaaaaaaac 720
tataaaataa ccatgaaaac caaaaaacta gaaaagttaa tttgaactca gaaaggaaca 780
caaacactat atgaattatt tgagcgtata tactaatgaa atagcatctg tttgtgcatc 840
aataatacca tcattattta agaaataaga agaagctaaa attcaa 886
```

<210> 119
<211> 236
<212> PRT
<213> human metapneumo virus

```
<400> 119
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65 70 75 80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100 105 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
115 120 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130 135 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145 150 155 160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165 170 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180 185 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195 200 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
```

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```

      210      215      220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225      230      235

```

```

<210> 120
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 120
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1      5      10      15
Ser Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20      25      30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35      40      45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50      55      60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65      70      75      80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85      90      95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100      105      110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
115      120      125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130      135      140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145      150      155      160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165      170      175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180      185      190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195      200      205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
210      215      220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225      230      235

```

```

<210> 121
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 121
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20      25      30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35      40      45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50      55      60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65      70      75      80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85      90      95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Asn Ser

```

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```

      100      105      110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
      115      120      125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
      130      135      140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145      150      155      160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
      165      170      175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Ala Gln
      180      185      190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195      200      205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
210      215      220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225      230      235

```

<210> 122
 <211> 236
 <212> PRT
 <213> human metapneumo virus

```

<400> 122
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
 1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
      20      25      30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
      35      40      45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
 50      55      60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65      70      75      80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
      85      90      95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Asn Ser
      100      105      110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asp Arg Pro Pro
      115      120      125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
      130      135      140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145      150      155      160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
      165      170      175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
      180      185      190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195      200      205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
210      215      220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225      230      235

```

<210> 123
 <211> 236
 <212> PRT
 <213> human metapneumo virus

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```

<400> 123
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20     25     30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35     40     45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50     55     60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65     70     75     80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85     90     95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100    105    110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asp Arg Pro Pro
115    120    125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130    135    140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Ile Ser Ser Arg Thr
145    150    155    160
His Ser Pro Pro Trp Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165    170    175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180    185    190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195    200    205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Thr Gln Arg Lys Ser Val
210    215    220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225    230    235

```

```

<210> 124
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 124
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20     25     30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35     40     45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
50     55     60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65     70     75     80
Pro Ile Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
85     90     95
Gln Ser Thr Glu Asp Ser Thr Leu His Ser Ala Ala Ser Ala Ser Ser
100    105    110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
115    120    125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Arg Thr
130    135    140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Val Ser Pro Arg Thr
145    150    155    160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
165    170    175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Leu Ser Thr Ala Ser Val Gln

```

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```

          180          185          190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Thr Ser Pro Val
          195          200          205
Ser Pro Gln Thr Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
          210          215          220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225          230          235

```

```

<210> 125
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 125
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
 1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
          65          70          75          80
Pro Met Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Gly Ser Thr Leu His Phe Ala Ala Ser Ala Ser Ser
          100          105          110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
          115          120          125
Phe Val Asp Thr His Thr Thr Pro Ser Ser Ala Ser Arg Thr Lys Thr
          130          135          140
Ser Pro Ala Val His Thr Lys Asn Asn Leu Arg Ile Ser Pro Arg Thr
          145          150          155          160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
          165          170          175
Leu Arg Thr Ser Ser Ile Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
          180          185          190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Ala Ser Pro Val
          195          200          205
Ser Pro Gln Ala Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
          210          215          220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225          230          235

```

```

<210> 126
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 126
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
 1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Met Gln Glu Asn Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val

```

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```

65          70          75          80
Pro Met Asp Asn Ser Asp Thr Asn Pro Gly Ser Gln Tyr Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Gly Ser Thr Leu His Phe Ala Ala Ser Ala Ser Ser
          100          105          110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Ser Arg Pro Pro
          115          120          125
Phe Val Asp Thr His Thr Thr Pro Ser Ser Ala Ser Arg Ile Arg Thr
          130          135          140
Ser Pro Ala Val His Thr Lys Asn Asn Leu Arg Ile Ser Pro Arg Thr
145          150          155          160
His Ser Pro Pro Trp Ala Met Thr Arg Thr Val Arg Gly Thr Thr Thr
          165          170          175
Leu Arg Thr Ser Ser Ile Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
          180          185          190
Pro Asp Ser Ser Ala Thr Thr His Lys His Glu Glu Ala Ser Pro Val
          195          200          205
Ser Pro Gln Ala Ser Ala Ser Thr Ala Arg Pro Gln Arg Lys Gly Met
210          215          220
Glu Ala Ser Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225          230          235

```

<210> 127

<211> 228

<212> PRT

<213> Human metapneumo virus

<220>

<221> VARIANT

<222> 220

<223> Xaa = unknown amino acid or other

<400> 127

```

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Pro Pro Thr Glu Pro Asn Lys Glu Ala Ser Thr Ile
65          70          75          80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Ser Ser Gln His Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
          100          105          110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
          115          120          125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
          130          135          140
Lys Pro Thr Val His Thr Ile Asn Asn Pro Asn Thr Ala Ser Ser Thr
145          150          155          160
Gln Ser Pro Pro Arg Thr Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
          165          170          175
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Leu Val Gln
          180          185          190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
          195          200          205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Asn
210          215          220

```

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Ile Lys Pro Asn
225

<210> 128
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 128
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
130 135 140
Lys Pro Thr Val His Thr Lys Asn Asn Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Thr Ser Thr Arg Lys Arg Pro Thr Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Ser Gln His Thr Asn Asn
210 215 220
Ile Lys Pro Asn
225

<210> 129
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 129
Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
65 70 75 80
Pro Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
100 105 110

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```

Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
      115      120      125
Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
      130      135      140
Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
      145      150      155      160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
      165      170      175
Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Ser Val Gln
      180      185      190
Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
      195      200      205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
      210      215      220
Thr Lys Gln Asn
225

```

```

<210> 130
<211> 228
<212> PRT
<213> human metapneumo virus

```

```

<220>
<221> VARIANT
<222> 81
<223> Xaa = Any Amino Acid

```

```

<400> 130
Met Glu Val Lys Val Glu Asn Ile Arg Ala Val Asp Met Leu Lys Ala
  1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
      20      25      30
Leu Ile Leu Val Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
      35      40      45
Leu Ile Val Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
      50      55      60
His Thr Ser Ser Ser Pro Thr Glu Ser Asn Lys Gly Thr Ser Thr Ile
      65      70      75      80
Xaa Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
      85      90      95
Gln Ser Thr Glu Ser Pro Thr Leu Asn Thr Ala Ala Ser Val Ser Pro
      100      105      110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
      115      120      125
Ser Ala Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
      130      135      140
Lys Leu Thr Val His Thr Lys Asn Asn Leu Ser Thr Ala Ser Arg Thr
      145      150      155      160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Val Leu Arg Asp Thr Ala
      165      170      175
Phe His Thr Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Ser Val Gln
      180      185      190
Ser Gly Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Ser Ser Ser
      195      200      205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asp Gln Asp Thr Asn Asn
      210      215      220
Thr Lys Gln Asn
225

```

```

<210> 131

```


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<211> 228
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 131
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Met Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
130 135 140
Lys Leu Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Ser Ile Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile
210 215 220
Val Lys Pro Asn
225

<210> 132
<211> 228
<212> PRT
<213> Human metapneumovirus

<220>
<221> VARIANT
<222> 220
<223> Xaa = unknown amino acid or other

<400> 132
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile

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```

65          70          75          80
Ser Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro
          100          105          110
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Ser Arg Leu Ser
          115          120          125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr
          130          135          140
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145          150          155          160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
          165          170          175
Phe Arg Thr Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln
          180          185          190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
          195          200          205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Thr Asn Ile
          210          215          220
Val Lys Pro Asn
225

```

<210> 133

<211> 228

<212> PRT

<213> Human metapneumovirus

<220>

<221> VARIANT

<222> 220

<223> Xaa = unknown amino acid or other

<400> 133

```

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65          70          75          80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Ser
          100          105          110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
          115          120          125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
          130          135          140
Lys Pro Thr Val His Thr Arg Asn Asn Pro Ser Thr Ala Ser Ser Thr
145          150          155          160
Gln Ser Pro Pro Arg Val Thr Thr Lys Ala Ile Leu Arg Ala Thr Val
          165          170          175
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Ala Thr Thr Leu Val Gln
          180          185          190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
          195          200          205
Asn Ser Gln Ala Ser Ala Ser Thr Met Gln Asn Xaa His Ser Asn Asn
210          215          220

```

WO 03/072719

PCT/US03/05271

Ile Lys Pro Asn
225

<210> 134
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 134
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Ser Ile Asp Asn Ser Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Ser Pro Thr Ala Ser Val Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Ser Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Ala Arg Thr
130 135 140
Lys Pro Thr Val His Lys Lys Asn Ile Pro Ser Thr Val Ser Arg Thr
145 150 155 160
Gln Ser Pro Leu Arg Ala Thr Thr Lys Ala Val Leu Arg Ala Thr Ala
165 170 175
Phe Arg Met Ser Ser Thr Gly Glu Gly Pro Thr Thr Thr Ser Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
210 215 220
Ala Lys Pro Asn
225

<210> 135
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 135
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65 70 75 80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
100 105 110

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Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
      115      120      125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
      130      135      140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
      145      150      155      160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
      165      170      175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
      180      185      190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
      195      200      205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
      210      215      220
Ala Arg Pro Asn
225

```

```

<210> 136
<211> 228
<212> PRT
<213> human metapneumo virus

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```

<400> 136
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
  1      5      10      15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
      20      25      30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
      35      40      45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
      50      55      60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
      65      70      75      80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
      85      90      95
Gln Ser Ala Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
      100      105      110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
      115      120      125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
      130      135      140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
      145      150      155      160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
      165      170      175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
      180      185      190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
      195      200      205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
      210      215      220
Ala Arg Pro Asn
225

```

```

<210> 137
<211> 228
<212> PRT
<213> human metapneumo virus

```

```

<400> 137

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```

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Thr Ser Thr Ile
65          70          75          80
Pro Ile Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Ser Leu Thr Leu Tyr Pro Thr Ser Ser Val Ser Ser
          100          105          110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Gly Ile Thr Asn His Leu Ser
          115          120          125
Phe Val Asp Arg Ser Thr Thr Gln Pro Ser Glu Ser Arg Thr Lys Thr
          130          135          140
Asn Arg Thr Val His Lys Lys Asn Ile Ser Ser Thr Val Ser Arg Thr
145          150          155          160
Gln Ser Pro Pro Arg Thr Thr Ala Lys Ala Val Pro Arg Ala Thr Ala
          165          170          175
Leu Arg Thr Ser Ser Thr Gly Glu Arg Pro Thr Thr Thr Pro Val Gln
          180          185          190
Pro Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
          195          200          205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Ile
210          215          220
Ala Arg Pro Asn
225

```

```

<210> 138
<211> 228
<212> PRT
<213> human metapneumo virus

```

```

<400> 138
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
 1          5          10          15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
          20          25          30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
          35          40          45
Leu Ile Ile Asn Tyr Thr Ile Gln Gln Thr Thr Ser Glu Ser Glu His
          50          55          60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65          70          75          80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
          85          90          95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
          100          105          110
Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
          115          120          125
Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
          130          135          140
Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
145          150          155          160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
          165          170          175
Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
180          185          190

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Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
210 215 220
Ile Lys Pro Asn
225

<210> 139
<211> 228
<212> PRT
<213> human metapneumo virus

<400> 139
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65 70 75 80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
100 105 110
Ser Glu Thr Glu Ser Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125
Ser Val Asp Arg Ser Thr Val Gln Pro Ser Glu Asn Arg Thr Lys Thr
130 135 140
Lys Leu Thr Val His Thr Arg Asn Asn Leu Ser Thr Ala Ser Ser Thr
145 150 155 160
Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
165 170 175
Leu Arg Met Ser Ser Thr Gly Arg Arg Pro Thr Thr Thr Leu Val Gln
180 185 190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn Gln His Thr Asn Asn
210 215 220
Ile Lys Pro Asn
225

<210> 140
<211> 231
<212> PRT
<213> Human metapneumo virus

<220>
<221> VARIANT
<222> 225
<223> Xaa = unknown amino acid or other

<400> 140
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1 5 10 15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20 25 30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe

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      35      40      45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
  50      55      60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
  65      70      75      80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
      85      90      95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro Glu Gly His
  100      105      110
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala Pro Gln Gln
  115      120      125
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn Glu Gln Ile
  130      135      140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr Gln Lys
  145      150      155      160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
      165      170      175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
  180      185      190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Thr Gln Ser Ser
  195      200      205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
  210      215      220
Xaa Arg Gly Ala Lys Leu Lys
  225      230

```

<210> 141
 <211> 231
 <212> PRT
 <213> human metapneumo virus

```

<400> 141
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1      5      10      15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
  35      40      45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
  50      55      60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
  65      70      75      80
Ser Thr Ala Gly Pro Ser Thr Glu Pro Asn Pro Gln Gln Ala Thr Gln
      85      90      95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Leu Glu Ser His
  100      105      110
Pro Tyr Thr Gly Thr Thr Gln Thr Pro Asp Ile Thr Ala Pro Gln Gln
  115      120      125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
  130      135      140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Lys
  145      150      155      160
Arg Glu Lys Glu Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
      165      170      175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Thr Arg Asn Ala Ser Glu Thr
  180      185      190
Ile Thr Thr Ser Asp Arg Pro Arg Ile Asp Thr Thr Thr Gln Ser Ser
  195      200      205
Asp Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
  210      215      220
Gln Ser Gly Ala Lys Pro Lys

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230

<210> 142
<211> 231
<212> PRT
<213> human metapneumo virus

<400> 142
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1 5 10 15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20 25 30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35 40 45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
50 55 60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65 70 75 80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85 90 95
Trp Thr Thr Glu Asn Ser Thr Phe Pro Ala Ala Thr Ser Glu Gly His
100 105 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
115 120 125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
130 135 140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145 150 155 160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
165 170 175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
180 185 190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
195 200 205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
210 215 220
Gln Gly Ser Ala Lys Pro Lys
225 230

<210> 143
<211> 231
<212> PRT
<213> human metapneumo virus

<400> 143
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1 5 10 15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20 25 30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35 40 45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
50 55 60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Arg Lys Thr Pro Met Thr
65 70 75 80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85 90 95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
100 105 110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln

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      115      120      125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
      130      135      140
Thr Gln Ala Thr Thr Glu Lys Lys Thr Thr Arg Glu Thr Thr Gln Arg
145      150      155      160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
      165      170      175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
      180      185      190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
      195      200      205
Glu Gln Thr Thr Gln Ala Thr Asp Pro Ser Ser Pro Ala His His Ala
      210      215      220
Gln Gly Ser Ala Lys Pro Lys
225      230

```

<210> 144
 <211> 231
 <212> PRT
 <213> human metapneumo virus

```

<400> 144
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1      5      10      15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
      35      40      45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
      50      55      60
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65      70      75      80
Ser Thr Ala Gly Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
      85      90      95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
      100      105      110
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
      115      120      125
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
      130      135      140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145      150      155      160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
      165      170      175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
      180      185      190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
      195      200      205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
      210      215      220
Gln Gly Ser Ala Lys Pro Lys
225      230

```

<210> 145
 <211> 231
 <212> PRT
 <213> human metapneumo virus

```

<400> 145
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala

```

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```

1           5           10           15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
20
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
50
Cys Ala Asn Met Pro Pro Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
65
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85
Trp Thr Thr Glu Asn Ser Thr Ser Pro Ala Ala Thr Pro Glu Gly His
100
Leu His Thr Gly Thr Thr Gln Thr Pro Asp Thr Thr Ala Pro Gln Gln
115
Thr Thr Asp Lys His Thr Ala Leu Pro Lys Ser Thr Asn Glu Gln Ile
130
Thr Gln Thr Thr Thr Glu Lys Lys Thr Thr Arg Ala Thr Thr Gln Arg
145
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
165
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ile Glu Thr
180
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Ser Thr Thr Gln Ser Ser
195
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser His Pro His His Ala
210
Gln Gly Ser Ala Lys Pro Lys
225
230

```

<210> 146

<211> 236

<212> PRT

<213> human metapneumo virus

<400> 146

```

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1           5           10           15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
20
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His
50
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
85
Leu Ala Ala Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
100
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
115
Thr Thr Asp Glu Tyr Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
130
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
165
Thr Thr Asn Gln Thr Ser Tyr Val Arg Glu Ala Thr Thr Thr Ser Ala
180
Arg Ser Arg Asn Ser Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
190

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```

      195      200      205
Ala Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
      210      215      220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225      230      235

```

```

<210> 147
<211> 236
<212> PRT
<213> Human metapneumo virus

```

```

<220>
<221> VARIANT
<222> 220, 227
<223> Xaa = unknown amino acid or other

```

```

<400> 147
Met Glu Val Arg Val Glu Asn Ile Arg Thr Ile Asp Met Phe Lys Ala
 1      5      10      15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
      35      40      45
Leu Ile Ile Asp Tyr Ala Thr Phe Lys Asn Met Thr Lys Val Glu His
      50      55      60
Cys Ala Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
      65      70      75      80
Ser Thr Val Asp Ser Ser Thr Gly Pro Asn Pro Gln Gln Thr Thr Gln
      85      90      95
Trp Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
      100      105      110
Leu His Thr Gly Thr Thr Pro Thr Leu Asp Ala Thr Val Ser Gln Gln
      115      120      125
Thr Pro Asp Lys His Thr Thr Pro Leu Arg Ser Thr Asn Gly Gln Thr
      130      135      140
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Arg Ala Ile Ala Lys Lys
      145      150      155      160
Glu Thr Thr Asn Gln Thr Thr Ser Thr Ala Ala Thr Gln Thr Phe Asn
      165      170      175
Thr Thr Asn Gln Thr Arg Asn Gly Arg Glu Thr Thr Ile Thr Ser Ala
      180      185      190
Arg Ser Arg Asn Asp Ala Thr Thr Gln Ser Ser Glu Gln Thr Asn Gln
      195      200      205
Thr Thr Asp Pro Ser Ser Gln Pro His His Ala Xaa Ile Ser Thr Ile
      210      215      220
Thr Ile Xaa Thr Gln His Arg His Ile Phe Ser Lys
225      230      235

```

```

<210> 148
<211> 236
<212> PRT
<213> Human metapneumo virus

```

```

<220>
<221> VARIANT
<222> 208
<223> Xaa = unknown amino acid or other

```

```

<400> 148
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala

```

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```

1           5           10           15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
20
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35
Leu Ile Ile Asp Tyr Ala Met Leu Lys Asn Met Thr Lys Val Glu His
50
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln
85
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Asp His
100
Leu Leu Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
115
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
130
Thr Gln Thr Thr Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
165
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Thr
180
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Thr Thr Xaa
195
Thr Ala Asp Pro Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
210
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225
230
235

```

<210> 149

<211> 236

<212> PRT

<213> human metapneumo virus

<400> 149

```

Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
1           5           10           15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
20
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
35
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
50
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65
Ser Ala Val Asp Leu Asn Thr Lys Leu Asn Pro Gln Gln Ala Thr Gln
85
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Ser Glu Gly His
100
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
115
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
130
Thr Gln Thr Ala Thr Glu Lys Lys Pro Thr Gly Ala Thr Thr Lys Lys
145
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Pro Asn
165
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
180
Arg Ser Arg Asn Gly Ala Thr Thr Gln Asn Ser Asp Gln Ile Thr Gln
195
200
205

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Ala Ala Asp Ser Ser Ser Gln Pro His His Thr Gln Lys Ser Thr Thr
  210      215      220
Thr Ala Tyr Asn Thr Asp Thr Ser Phe Pro Ser Ser
  225      230      235

```

```

<210> 150
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 150
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1      5      10      15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
      35      40      45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
      50      55      60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
      65      70      75      80
Ser Ala Val Asp Ser Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
      85      90      95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Asp His
      100      105      110
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
      115      120      125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
      130      135      140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
      145      150      155      160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
      165      170      175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
      180      185      190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
      195      200      205
Ala Ala Glu Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr
      210      215      220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Leu Ser Ser
      225      230      235

```

```

<210> 151
<211> 236
<212> PRT
<213> human metapneumo virus

```

```

<400> 151
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1      5      10      15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Ser Ala Leu Ser Met Ala Leu Asn Ile Phe
      35      40      45
Leu Ile Ile Asp Tyr Ala Lys Ser Lys Asn Met Thr Arg Val Glu His
      50      55      60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
      65      70      75      80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Arg Ala Thr Gln
      85      90      95

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Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Gly His
      100      105
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Val Thr Val Ser Gln Gln
      115      120
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
      130      135      140
Thr Gln Thr Ala Ala Glu Lys Lys Pro Thr Arg Val Thr Thr Asn Lys
145      150      155      160
Glu Thr Ile Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
      165      170      175
Thr Thr Asn Gln Thr Asn Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
      180      185      190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
      195      200      205
Ala Ala Asp Pro Ser Ser Gln Ser Gln His Thr Gln Lys Ser Ile Thr
      210      215      220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225      230      235

```

```

<210> 152
<211> 236
<212> PRT
<213> human metapneumo virus

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<400> 152
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
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Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
      20      25      30
Leu Ile Leu Ile Gly Leu Ser Ala Leu Ser Met Ala Leu Asn Ile Phe
      35      40      45
Leu Ile Ile Asp Tyr Ala Lys Ser Lys Thr Met Thr Arg Val Glu His
      50      55      60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65      70      75      80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
      85      90      95
Leu Thr Thr Glu Asp Ser Thr Ser Pro Ala Ala Thr Leu Glu Gly His
      100      105      110
Leu His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
      115      120      125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
      130      135      140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
145      150      155      160
Glu Thr Ile Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
      165      170      175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
      180      185      190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
      195      200      205
Ala Ala Asp Pro Ser Ser Gln Ser Gln His Thr Lys Lys Ser Thr Thr
      210      215      220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Pro Ser Ser
225      230      235

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<210> 153
<211> 236
<212> PRT
<213> human metapneumo virus

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<400> 153

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Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
 1           5           10           15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
           20           25           30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
           35           40           45
Leu Ile Ile Asp Tyr Ala Thr Leu Lys Asn Met Thr Lys Val Glu His
           50           55           60
Cys Val Asn Met Pro Pro Val Glu Pro Ser Lys Lys Thr Pro Met Thr
65           70           75           80
Ser Ala Val Asp Leu Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
           85           90           95
Leu Thr Thr Glu Asp Ser Thr Ser Leu Ala Ala Thr Leu Glu Asp His
           100          105          110
Pro His Thr Gly Thr Thr Pro Thr Pro Asp Ala Thr Val Ser Gln Gln
           115          120          125
Thr Thr Asp Glu His Thr Thr Leu Leu Arg Ser Thr Asn Arg Gln Thr
           130          135          140
Thr Gln Thr Thr Ala Glu Lys Lys Pro Thr Arg Ala Thr Thr Lys Lys
145           150           155           160
Glu Thr Thr Thr Arg Thr Thr Ser Thr Ala Ala Thr Gln Thr Leu Asn
           165          170          175
Thr Thr Asn Gln Thr Ser Asn Gly Arg Glu Ala Thr Thr Thr Ser Ala
           180          185          190
Arg Ser Arg Asn Asn Ala Thr Thr Gln Ser Ser Asp Gln Thr Thr Gln
           195          200          205
Ala Ala Glu Pro Asn Ser Gln Ser Gln His Thr Gln Lys Ser Thr Thr
           210          215          220
Thr Thr Tyr Asn Thr Asp Thr Ser Ser Leu Ser Ser
225           230           235

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<210> 154

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 154

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gcttgccctct taagagaaga ccaaggatgg tattgtcaaa atgcaggggtc aactgtttac 180
taccctaatg aaaaagactg tgaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

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<210> 155

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 155

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gcttgccctct taagagaaga tcaaggatgg tattgtcaga atgcaggggtc aactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

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<210> 156
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 156
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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagattg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtggc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 157
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 157
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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449

<210> 158
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 158
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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagattg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449

<210> 159
<211> 449
<212> DNA
<213> human metapneumo virus

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gcttgccctc taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg tgaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
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<210> 160
<211> 449

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<212> DNA
<213> human metapneumo virus

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taccctaatg aaaaagactg tgaacaaga ggagaccatg tcttttgca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449

<210> 161
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 161
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gcttgccctt taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg tgaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 162
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 162
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gacacgcctt gctggatagt aaaagcagcc cttcttctgtt cagaaaaaaa gggaaactat 120
gcttgccctt taagagaaga tcaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg tgaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtaggaatc 420
atcaagcaac tgaacaaagg ctgctctta 449

<210> 163
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 163
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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
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<210> 164
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 164
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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449
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<210> 165
<211> 449
<212> DNA
<213> human metapneumo virus
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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 166
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 166
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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca atatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 167
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 167
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gcttgccctt taagagaaga tcaaagatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449
```

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<210> 168
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 168
ataggagttt atggaagctc cgtaatttac atggtgcaac tgccaatctt tggagttata 60
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gacacgcctt gctggatagt aaaagcggcc ctttcttgct cagaaaaaaa gggaaactat 120
gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttctattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

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<210> 169

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 169

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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

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<210> 170

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 170

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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctttggttg cttgctacaa gggagtgagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449

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<210> 171

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 171

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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449

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<210> 172

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 172

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gcttgccctt taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180

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tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcca cacagcagca 240
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 173
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 173
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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactgtc tcctcttggg 360
gctttgggtt cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 174
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 174
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gcttgccctc taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
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atcaagcaac tgaacaaagg ctgctctta 449
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<210> 175
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 175
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gcttgccctc taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg tgaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcactatc tcctcttggg 360
gctttgggtt cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 176
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 176
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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgcca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
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ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctttgggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 177

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 177

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gacacgcctt gctggatagt aaaagcagcc ccttcttgct cagaaaaaaa gggaaactat 120
gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctctgggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 178

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 178

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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac cactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctttgggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 179

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 179

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gcttgccctc taagagaaga tcaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg aaaaagactg cgaaacaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacatca acatatccac cactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactgtc tcctcttggg 360
gctttgggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
atcaagcaac tgaacaaagg ctgctctta 449
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<210> 180

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 180

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gacacgcctt gctggatagt aaaagcagcc ccttcttggt caggaaaaaa gggaaactat 120
gcttgccctc taagagaaga ccaaggatgg tattgtcaaa atgcagggtc aactgtttac 180
taccctaatg aaaaagactg tgaacaaaga ggagaccatg tcttttgca cacagcagca 240
ggaatcaatg ttgctgagca gtcaaaggag tgcaacataa acatatctac tactaattac 300
ccatgcaaag ttagcacagg aagacatcct atcagtatgg ttgcaactatc tcctcttggg 360
gctttgggttg cttgctacaa gggagtggagc tgttccattg gcagcaacag agtagggatc 420
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atcaagcaac tgaacaaagg ctgctctta

449

<210> 181

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 181

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gcttgccctc	taagagaaga	tcaaggatgg	tattgtcaga	atgcagggtc	aactgtttac	180
tacccaaatg	aaaaagactg	cgaacaaga	ggagaccatg	tcttttgca	cacagcagca	240
ggaatcaatg	ttgctgagca	gtcaaaggag	tgcaacatca	acatatccac	tactaattac	300
ccatgcaaag	ttagcacagg	aagacatcct	atcagtatgg	ttgcaactgc	tcctcttggg	360
gctttggttg	cttgctacaa	gggagtgaag	tggtccattg	gcagcaacag	agtagggatc	420
atcaagcaac	tgaacaaagg	ctgctctta				449

<210> 182

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 182

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gcttgccctc	taagagaaga	ccaaggatgg	tattgtcaaa	atgcagggtc	aactgtttac	180
tacccaaatg	aaaaagactg	tgaacaaga	ggagaccatg	tcttttgca	cacagcagca	240
ggaatcaatg	ttgctgagca	gtcaaaggag	tgcaacataa	acatatctac	tactaattac	300
ccatgcaaag	ttagcacagg	aagacatcct	atcagtatgg	ttgcaactatc	tcctcttggg	360
gctttggttg	cttgctacaa	gggagtgaag	tggtccattg	gcagcaacag	agtagggatc	420
atcaagcaac	tgaacaaagg	ctgctctta				449

<210> 183

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 183

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gacacgcctt	gctggatagt	aaaagcagcc	ccctcttggt	ccgaaaaaaa	gggaaactat	120
gcttgccctc	taagagaaga	ccaagggtgg	tattgtcaga	atgcagggtc	aactgtttac	180
tacccaaatg	agaaagactg	tgaacaaga	ggagaccatg	tcttttgca	cacagcagca	240
ggaatcaatg	ttgctgagca	atcaaaggag	tgcaacatca	acatatccac	tacaaattac	300
ccatgcaaag	tcagcacagg	aagacatcct	atcagtatgg	ttgcaactgc	ccctcttggg	360
gctctggttg	cttgctacaa	aggagtaagc	tggtccattg	gcagcaatag	agtagggatt	420
atcaagcagc	tgaacaaagg	ttgctctta				449

<210> 184

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 184

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gacacgcctt	gctggatagt	aaaagcagcc	ccctcttggt	ccgaaaaaaa	gggaaactat	120
gcttgccctt	taagagaaga	tcaagggtgg	tattgtcaga	atgcagggtc	aactgtttac	180
tacccaaatg	agaaagactg	tgaacaaga	ggagaccatg	tcttttgca	cacagcagca	240
ggaatcaatg	ttgctgagca	atcaaaagag	tgcaacatca	acatatccac	tacaaattac	300
ccatgcaaag	tcagcacagg	aagacatcct	atcagtatgg	ttgcaactgc	ccctcttggg	360
gctctagttg	cttgctacaa	aggagtaagc	tggtccattg	gcagcaatag	agtagggatc	420
atcaagcagc	tgaacaaagg	ttgctccta				449

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<210> 185
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 185
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gacacgcctt gctggatagt aaaagcagcc cctcttggtt ccgaaaaaaa gggaaactat 120
gcttgccctt taagagaaga tcaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagtagca 240
ggaattaatg ttgctgagca atcaaaagag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc ccctcttggg 360
gctctagttg cttgctacaa aggagtaagc tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449
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<210> 186
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 186
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gacacgcctt gctggatagt aaaagcagcc cctcttggtt ccgaaaaaaa gggaaactat 120
gcttgccctt taagagaaga tcaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaagag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc ccctcttggg 360
gctctagttg cttgctacaa aggagtaagc tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449
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<210> 187
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 187
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gacacgcctt gctggatagt aaaagcagcc cctcttggtt ccgaaaaaaa gggaaactat 120
gcttgccctt taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaggactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaaggag tgcaacatca acatatccac cacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgactgtc ccctcttggg 360
gctctggttg cttgttaciaa aggagtaagc tgttctattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta 449
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<210> 188
<211> 449
<212> DNA
<213> human metapneumo virus

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<400> 188
ataggggtct acgggagctc cgtaattttac atggtgcagc tgccaatctt tggcgttata 60
gacacgcctt gctggatagt aaaagcagcc cctcttggtt ccgaaaaaaa gggaaactat 120
gcttgccctt taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaaggag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctctagttg cttgctacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449
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<210> 189
<211> 449

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<212> DNA
<213> human metapneumo virus

<400> 189
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gacacgcctt gctggatagt aaaagcagcc ccttcttggt ccgaaaaaaa gggaaactat 120
gcttgccctc taagagaaga ccaaggggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaaatg agaaggactg tgaacaaga ggagaccatg tcttttgoga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgactgtc ccctctggg 360
gctctggttg cttgttaca aggagtaagc tgttctattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta 449

<210> 190
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 190
ataggggtct acgggagctc cgtaattttac atgggtgcagc tgccaatctt tggcggttata 60
gacacgcctt gctggatagt aaaagcagcc ccttcttggt ccgaaaaaaa gggaaactat 120
gcttgccctc taagagaaga ccaaggggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaaatg agaaggactg tgaacaaga ggagaccatg tcttttgoga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctctggttg cttgttaca aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449

<210> 191
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 191
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gcttgccctc taagagaaga ccaaggggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaaatg agaaggactg tgaacaaga ggagaccatg tcttttgoga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac tacaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctctggttg cttgttaca aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449

<210> 192
<211> 449
<212> DNA
<213> human metapneumo virus

<400> 192
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gcttgccctc taagagaaga ccaaggatgg tattgtcaga atgcagggtc aactgtttac 180
taccctaaatg agaaggactg tgaacaaga ggagaccatg tcttttgoga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac cacaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgactgtc ccctctggg 360
gctctggttg cttgttaca aggagtaagt tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta 449

<210> 193
<211> 449
<212> DNA
<213> human metapneumo virus

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gcttgccctc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac taaaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
gctctggttg cttgtacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
ataaagcagc tgaacaaagg ttgctccta 449
```

```
<210> 194
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 194
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gacacgcctt gctggatagt aaaagcagcc cttcttggt ccgaaaaaaa gggaaactat 120
gcttgccctc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggag tgcaacatca acatatccac caaaaattac 300
ccatgcaaag tcagcacagg aaggcatcct atcagtatgg ttgactgtc ccctctcggg 360
gctctggttg cctgttacia aggagtaagt tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta 449
```

```
<210> 195
<211> 449
<212> DNA
<213> human metapneumo virus
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```
<400> 195
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gacacacctt gctggatagt aaaagcagcc cttcttggt ccgaaaaaaa gggaaattat 120
gcttgccctc taagagaaga ccaagggtgg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgcga cacagcagca 240
ggaattaatg ttgctgagca atcaaaggaa tgcaacatca acatatccac taaaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tcctcttggg 360
gctctggttg cttgtacaa aggagtaagc tgttccattg gcagcaacag agtagggatc 420
atcaagcagc tgaacaaagg ttgctccta 449
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<210> 196
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 196
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gctctggttg cctgttacia aggagtaagt tgttccattg gcagcaatag agtagggatc 420
atcaagcagc tgaacaaagg ttgctctta 449
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```
<210> 197
<211> 449
<212> DNA
<213> human metapneumo virus
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```
<400> 197
ataggggtct acgggagctc cgtaattttac atggtgcagc tgccaatctt tggcggttata 60
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gacacgcctt gctggatagt aaaagcagcc ccttcttggt cggaaaaaaa gggaaactat 120
gcttgccctc taagagaaga ccaaggggtg tattgtcaga atgcagggtc aactgtttac 180
taccctaatg agaaagactg tgaacaaga ggagaccatg tcttttgga cacagcagca 240
ggaattaatg ttgctgagca atcaaggag tgcaacatca acatatccac taaaattac 300
ccatgcaaag tcagcacagg aagacatcct atcagtatgg ttgactgtc tctcttggg 360
gctctggttg cttgctataa aggagtaagc tgttcattg gcagcaacag agtagggatc 420
ataaagcagc tgaacaagg ttgctccta 449

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<210> 198

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 198

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gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgactatc acctctcgg 360
gctttggttg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat taccctaaagg ctgctcata 449

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<210> 199

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 199

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ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
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gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc tactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgga cacagcagca 240
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ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgactatc acctctcgg 360
gctttggttg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat taccctaaagg ctgctcata 449

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<210> 200

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 200

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gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc tactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgactatc acctctcgg 360
gctttggttg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat taccctaaagg ctgctcata 449

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<210> 201

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 201

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gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc tactgtttac 180

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ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaaac 420
atcaacaat tacccaaagg ctgctcata 449
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<210> 202
<211> 449
<212> DNA
<213> human metapneumo virus
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<400> 202
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaagggtgg tattgcaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaaac 420
atcaacaat tacctaaagg ctgctcata 449
```

```
<210> 203
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 203
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaaac 420
atcaacaat tacctaaagg ctgctcata 449
```

```
<210> 204
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 204
ataggggtct acggaagctc tgtaatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaaac 420
atcaacaat tacctaaagg ctgctcata 449
```

```
<210> 205
<211> 449
<212> DNA
<213> human metapneumo virus
```

```
<400> 205
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
```

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```
ccatgcaaag tcagcacagg aagacactct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 206

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 206

```
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cggaattat 120
gcttgctctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 207

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 207

```
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cggaattat 120
gcttgctctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg tgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 208

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 208

```
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cggaattat 120
gcttgctctc taagagagga tcaagggtgg tactgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 209

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 209

```
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tggggtcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cggaattat 120
gcttgctctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga tacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttggaatc 420
```

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atcaaacaat tacccaaagg ctgctcata

449

<210> 210

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 210

```
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagcc cctctttgct cagagaaaaa cgggaattat 120
gcttgccctcc taagagagga tcaaggggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tgtttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgggaatt 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 211

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 211

```
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctttgct cagagaaaaa cgggaattat 120
gcttgccctcc taagagagga tcaaggggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tgtttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 212

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 212

```
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctttgct cagaaaaaaa cgggaattat 120
gcttgccctcc taagagagga tcaaggggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg tgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

<210> 213

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 213

```
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctttgct cagaaaaaaa cgggaattat 120
gcttgccctcc taagagagga tcaaggggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgggaatc 420
atcaaacaat tacctaaagg ctgctcata 449
```

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<210> 214
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 214
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gatacacctt gttggataat caaggcagct ccctcttgct cagagaaaaa cgggaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg tgttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat tacctaaagg ctgctcata 449
```

<210> 215
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 215
ataggggtct acggaagctc tgtgatttac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga tacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat taccctaaagg ctgctcata 449
```

<210> 216
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 216
ataggggtct acggaagctc cgtgatttac atggttcaat tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttgct cagaaaaaaa cgggaattat 120
gcttgccctc taagagagga tcaaggggtg tactgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct ataagcatgg ttgcactatc acctctcggt 360
gctttggtgg cttgctataa aggggtaagc tgctcgattg gcagcaatcg ggttgaatc 420
atcaacaat tacctaaagg ctgctcata 449
```

<210> 217
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 217
ataggggtct acggaagctc tgtgatttac atggtccagc tgccgatctt tgggtgcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgcaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctataa gggggttagc tgctcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 218
<211> 449

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<212> DNA

<213> human metapneumo virus

<400> 218

```
ataggggtct acggaagctc tgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctctgtt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttggaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 219

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 219

```
ataggggtct acggaagctc tgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctctgtt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttggaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 220

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 220

```
ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctctgtt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga ccaagggtgg tattgtaaaa atgcgggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttggaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 221

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 221

```
ataggggtct acggaagctc cgtgatttac atgggtccagc taccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctctctgtt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactgtc acctctcggc 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttggaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 222

<211> 449

<212> DNA

<213> human metapneumo virus

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```
<400> 222
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gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac taccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 223

<211> 449

<212> DNA

<213> human metapneumo virus

```
<400> 223
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg tgaaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 224

<211> 449

<212> DNA

<213> human metapneumo virus

```
<400> 224
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga ccaagggtgg tattgtaaaa atgcgggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 225

<211> 449

<212> DNA

<213> human metapneumo virus

```
<400> 225
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
taccctaatg aaaaagactg cgaacaaga ggtgatcatg tttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 226

<211> 449

<212> DNA

<213> human metapneumo virus

```
<400> 226
ataggggtct acggaagctc cgtgatttac atggtccagc tgccgatctt tgggtgtcata 60
```


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```

gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg tgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttggaaata 420
atcaacaac tacctaaagg ctgctcata 449

```

<210> 227

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 227

```

ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcaattg gcagtaatcg ggttggaaata 420
atcaacaac tacctaaagg ctgctcata 449

```

<210> 228

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 228

```

ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcaattg gcagtaatcg ggttggaaata 420
atcaacaac tacctaaagg ctgctcata 449

```

<210> 229

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 229

```

ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180
taccctaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcactatc acctctcggt 360
gctttggtag cttgctacaa ggggttagc tgttcgattg gcagtaatcg ggttggaaata 420
atcaacaac tacctaaagg ctgctcata 449

```

<210> 230

<211> 449

<212> DNA

<213> human metapneumo virus

<400> 230

```

ataggggtct acggaagctc tgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct ccctcttggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaaggggtg tattgtaaaa atgcaggatc cactgtttac 180

```

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```
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatccac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactgc acctctcggc 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 231
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 231
ataggggtct acggaagctc tgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctcttgggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaacg ttgctgagca atcaagagaa tgcaacatca acatatctac caccaactat 300
ccgtgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactat acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgctcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 232
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 232
ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctcttgggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagctgca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactat acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcaattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 233
<211> 449
<212> DNA
<213> human metapneumo virus

```
<400> 233
ataggggtct acggaagctc cgtgatttac atgggtccagc tgccgatctt tgggtgtcata 60
gatacacctt gttggataat caaggcagct cctcttgggt cagaaaaaga tggaaattat 120
gcttgccctc taagagagga tcaagggtgg tattgtaaaa atgcaggatc cactgtttac 180
tacccaaatg aaaaagactg cgaaacaaga ggtgatcatg ttttttgtga cacagcagca 240
gggatcaatg ttgctgagca atcaagagaa tgcaacatca acatatctac aaccaactac 300
ccatgcaaag tcagcacagg aagacaccct atcagcatgg ttgcaactat acctctcggt 360
gctttggtag cttgctacaa aggggttagc tgttcgattg gcagtaatcg ggttgaata 420
atcaacaac tacctaaagg ctgctcata 449
```

<210> 234
<211> 149
<212> PRT
<213> human metapneumo virus

```
<400> 234
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
```

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```

          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
  50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
  65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145

```

```

<210> 235
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 235
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
  65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145

```

```

<210> 236
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 236
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
  65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser

```

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```

      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 237
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 237
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 238
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 238
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu

```

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130 135 140
Asn Lys Gly Cys Ser
145

<210> 239
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 239
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 240
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 240
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 241

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<211> 149
<212> PRT
<213> human metapneumo virus

<400> 241
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 242
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 242
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 243
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 243
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile

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```

1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130          135          140
Asn Lys Gly Cys Ser
145

```

```

<210> 244
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 244
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130          135          140
Asn Lys Gly Cys Ser
145

```

```

<210> 245
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 245
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu

```

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```

      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

```

<210> 246
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 246
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

```

<210> 247
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 247
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Arg Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser

```


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```

          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145

```

<210> 248
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 248
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20     25     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35     40     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50     55     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65     70     75     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85     90     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100    105    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115    120    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130    135    140
Asn Lys Gly Cys Ser
145

```

<210> 249
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 249
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20     25     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35     40     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50     55     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65     70     75     80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85     90     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100    105    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115    120    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130    135    140
Asn Lys Gly Cys Ser

```

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145

<210> 250
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 250
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 251
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 251
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 252
<211> 149
<212> PRT

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PCT/US03/05271

<213> human metapneumo virus

<400> 252

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145
```

<210> 253

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 253

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145
```

<210> 254

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 254

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
```

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```

                20                25                30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                40                45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                55                60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70                75                80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85                90                95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100                105                110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115                120                125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                135                140
Asn Lys Gly Cys Ser
145

```

```

<210> 255
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 255
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

```

<210> 256
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 256
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala

```

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```

65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100         105         110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115         120         125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130         135         140
Asn Lys Gly Cys Ser
145

```

<210> 257
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 257
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100         105         110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115         120         125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130         135         140
Asn Lys Gly Cys Ser
145

```

<210> 258
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 258
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100         105         110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly

```

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```

      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

```

<210> 259
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 259
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

```

<210> 260
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 260
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

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<210> 261
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 261
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 262
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 262
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 263
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 263

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```

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
           35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
           50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
           85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
           100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130          135          140
Asn Lys Gly Cys Ser
145

```

<210> 264
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 264
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
           35           40           45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
           50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
           85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
           100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130          135          140
Asn Lys Gly Cys Ser
145

```

<210> 265
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 265
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
           35           40           45

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```

Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Val Ala
 65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145

```

<210> 266
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 266
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Asn Lys Gly Cys Ser
145

```

<210> 267
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 267
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
          85          90          95

```

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```

Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 268
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 268
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 269
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 269
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140

```

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Asn Lys Gly Cys Ser
145

<210> 270
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 270
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 271
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 271
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 272
<211> 149

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PCT/US03/05271

<212> PRT
<213> human metapneumo virus

<400> 272
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 273
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 273
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Asn Lys Gly Cys Ser
145

<210> 274
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 274
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15

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```

Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 275
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 275
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Asn Lys Gly Cys Ser
145

```

<210> 276
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 276
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60

```

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```

Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100     105     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115     120     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130     135     140
Asn Lys Gly Cys Ser
145

```

```

<210> 277
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 277
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala Ala Pro Ser
      20     25     30
Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35     40     45
Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50     55     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile Asn Ile Ser
      85     90     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100    105    110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115    120    125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130    135    140
Asn Lys Gly Cys Ser
145

```

```

<210> 278
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 278
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20     25     30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35     40     45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50     55     60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85     90     95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100    105    110

```

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```

Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

```

<210> 279
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 279
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Trp Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

```

<210> 280
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 280
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

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<210> 281
 <211> 149
 <212> PRT
 <213> human metapneumo virus

<400> 281
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 282
 <211> 149
 <212> PRT
 <213> human metapneumo virus

<400> 282
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 283
 <211> 149
 <212> PRT
 <213> human metapneumo virus

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```

<400> 283
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
           35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
           50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
           65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
           85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
           100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
           130          135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 284
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 284
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
           35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
           50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
           65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
           85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
           100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
           115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
           130          135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 285
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 285
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
           20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln

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```

          35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
  50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
  65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Ser Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Pro Lys Gly Cys Ser
145

```

<210> 286
<211> 149
<212> PRT
<213> human metapneumo virus

```

<400> 286
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Pro Lys Gly Cys Ser
145

```

<210> 287
<211> 149
<212> PRT
<213> human metapneumo virus

```

<400> 287
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser

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```

      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

<210> 288

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 288

```

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

<210> 289

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 289

```

Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu

```

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130 135 140
Pro Lys Gly Cys Ser
145

<210> 290
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 290
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 291
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 291
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 292

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<211> 149
 <212> PRT
 <213> human metapneumo virus

<400> 292
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 293
 <211> 149
 <212> PRT
 <213> human metapneumo virus

<400> 293
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1 5 10 15
 Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20 25 30
 Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35 40 45
 Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50 55 60
 Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65 70 75 80
 Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85 90 95
 Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100 105 110
 Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115 120 125
 Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130 135 140
 Pro Lys Gly Cys Ser
 145

<210> 294
 <211> 149
 <212> PRT
 <213> human metapneumo virus

<400> 294
 Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile

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```

1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
                35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
                50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
                115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130                135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 295
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 295
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
                35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
                50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65                70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
                85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
                100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
                115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130                135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 296
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 296
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
                20           25           30
Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
                35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu

```

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```

      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

<210> 297
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 297
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100      105      110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115      120      125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130      135      140
Pro Lys Gly Cys Ser
145

```

<210> 298
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 298
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser

```

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PCT/US03/05271

```

          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 299
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 299
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100     105     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115     120     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130     135     140
Pro Lys Gly Cys Ser
145

```

```

<210> 300
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 300
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1      5      10      15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20      25      30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35      40      45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50      55      60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65      70      75      80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85      90      95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100     105     110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115     120     125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130     135     140
Pro Lys Gly Cys Ser

```


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PCT/US03/05271

145

<210> 301
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 301
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 302
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 302
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 303
<211> 149
<212> PRT

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<213> human metapneumo virus

<400> 303

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20           25           30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130          135          140
Pro Lys Gly Cys Ser
145
```

<210> 304

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 304

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
 20           25           30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
 35           40           45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
 50           55           60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
 65           70           75           80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
 85           90           95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
 100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
 115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
 130          135          140
Pro Lys Gly Cys Ser
145
```

<210> 305

<211> 149

<212> PRT

<213> human metapneumo virus

<400> 305

```
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1           5           10           15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
```

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```

                20                25                30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                40                45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                55                60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65                70                75                80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85                90                95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100                105                110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115                120                125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                135                140
Pro Lys Gly Cys Ser
145

```

<210> 306
<211> 149
<212> PRT
<213> human metapneumo virus

```

<400> 306
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1                5                10                15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20                25                30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                40                45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                55                60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65                70                75                80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85                90                95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100                105                110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115                120                125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130                135                140
Pro Lys Gly Cys Ser
145

```

<210> 307
<211> 149
<212> PRT
<213> human metapneumo virus

```

<400> 307
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1                5                10                15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20                25                30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35                40                45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50                55                60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala

```

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```

65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Pro Lys Gly Cys Ser
145

```

<210> 308
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 308
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
          130          135          140
Pro Lys Gly Cys Ser
145

```

<210> 309
 <211> 149
 <212> PRT
 <213> human metapneumo virus

```

<400> 309
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
  1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
          20          25          30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
          35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
          50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
          65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
          85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
          100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly

```

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```

          115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130          135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 310
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 310
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20          25          30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130          135          140
Pro Lys Gly Cys Ser
145

```

```

<210> 311
<211> 149
<212> PRT
<213> human metapneumo virus

```

```

<400> 311
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
 1          5          10          15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
      20          25          30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
      35          40          45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
      50          55          60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
      65          70          75          80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
      85          90          95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
      100          105          110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
      115          120          125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
      130          135          140
Pro Lys Gly Cys Ser
145

```

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<210> 312
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 312
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 313
<211> 149
<212> PRT
<213> human metapneumo virus

<400> 313
Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln Leu Pro Ile
1 5 10 15
Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala Ala Pro Ser
20 25 30
Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg Glu Asp Gln
35 40 45
Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr Pro Asn Glu
50 55 60
Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp Thr Ala Ala
65 70 75 80
Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile Asn Ile Ser
85 90 95
Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His Pro Ile Ser
100 105 110
Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys Tyr Lys Gly
115 120 125
Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile Lys Gln Leu
130 135 140
Pro Lys Gly Cys Ser
145

<210> 314
<211> 539
<212> PRT
<213> human metapneumo virus

<400> 314

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```

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1      5      10      15
His Gly Leu Lys Glu Ser Tyr Leu Glu Ser Cys Ser Thr Ile Thr
 20      25      30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ala Asp Gly Pro
 50      55      60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65      70      75      80
Leu Arg Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85      90      95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100      105      110
Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115      120      125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Lys Thr
130      135      140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145      150      155      160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165      170      175
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
180      185      190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195      200      205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210      215      220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225      230      235      240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245      250      255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260      265      270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275      280      285
Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290      295      300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305      310      315      320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325      330      335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340      345      350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355      360      365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370      375      380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385      390      395      400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
405      410      415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
420      425      430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
435      440      445
Val Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
450      455      460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465      470      475      480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
485      490      495

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```

Leu Ile Ala Val Leu Gly Ser Thr Met Ile Leu Val Ser Val Phe Ile
      500      505      510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
      515      520      525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Asn
      530      535

```

```

<210> 315
<211> 539
<212> PRT
<213> human metapneumo virus

```

```

<400> 315
Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
 1      5      10      15
His Gly Leu Lys Glu Ser Tyr Leu Glu Ser Cys Ser Thr Ile Thr
 20      25      30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
 35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
 50      55      60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
 65      70      75      80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
 85      90      95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100      105      110
Ala Thr Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115      120      125
Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Thr Thr
130      135      140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145      150      155      160
Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165      170      175
Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180      185      190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195      200      205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210      215      220
Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225      230      235      240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245      250      255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Thr Val Gln
260      265      270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275      280      285
Ala Pro Ser Cys Ser Glu Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290      295      300
Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305      310      315      320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325      330      335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340      345      350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355      360      365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370      375      380

```


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```

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385                               390                               395                               400
Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
                               405                               410                               415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
                               420                               425                               430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
                               435                               440                               445
Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
                               450                               455                               460
Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465                               470                               475                               480
Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
                               485                               490                               495
Leu Ile Ala Val Leu Gly Ser Ser Met Ile Leu Val Ser Ile Phe Ile
                               500                               505                               510
Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
                               515                               520                               525
Gly Val Thr Asn Asn Gly Phe Ile Pro His Ser
530                               535

```

<210> 316
 <211> 539
 <212> PRT
 <213> human metapneumo virus

```

<400> 316
Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
1                               5                               10                               15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
                               20                               25                               30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
                               35                               40                               45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
50                               55                               60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65                               70                               75                               80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
                               85                               90                               95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100                               105                               110
Ala Thr Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
115                               120                               125
Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Gln Thr
130                               135                               140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
145                               150                               155                               160
Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
                               165                               170                               175
Ile Asn Arg Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
180                               185                               190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195                               200                               205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210                               215                               220
Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
225                               230                               235                               240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
                               245                               250                               255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260                               265                               270

```

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```

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
      275      280      285
Ala Pro Ser Cys Ser Glu Lys Asn Gly Asn Tyr Ala Cys Leu Leu Arg
      290      295      300
Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
      305      310      315      320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
      325      330      335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
      340      345      350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
      355      360      365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
      370      375      380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Trp Val Gly Ile Ile
      385      390      395      400
Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
      405      410      415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
      420      425      430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
      435      440      445
Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
      450      455      460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
      465      470      475      480
Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Val Ile
      485      490      495
Leu Val Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
      500      505      510
Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
      515      520      525
Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
      530      535

```

<210> 317
 <211> 539
 <212> PRT
 <213> human metapneumo virus

```

<400> 317
Met Ser Trp Lys Val Met Ile Ile Ile Ser Leu Leu Ile Thr Pro Gln
  1      5      10      15
His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
      20      25      30
Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
      35      40      45
Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Thr Asp Gly Pro
      50      55      60
Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
      65      70      75      80
Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
      85      90      95
Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
      100      105      110
Ala Thr Ala Ala Ala Val Thr Ala Gly Ile Ala Ile Ala Lys Thr Ile
      115      120      125
Arg Leu Glu Ser Glu Val Asn Ala Ile Lys Gly Ala Leu Lys Thr Thr
      130      135      140
Asn Glu Ala Val Ser Thr Leu Gly Asn Gly Val Arg Val Leu Ala Thr
      145      150      155      160

```

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```

Ala Val Arg Glu Leu Lys Glu Phe Val Ser Lys Asn Leu Thr Ser Ala
165 170
Ile Asn Lys Asn Lys Cys Asp Ile Ala Asp Leu Lys Met Ala Val Ser
180 185 190
Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205
Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220
Ala Glu Leu Ala Arg Ala Val Ser Tyr Met Pro Thr Ser Ala Gly Gln
225 230 235 240
Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255
Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260 265 270
Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Ile Lys Ala
275 280 285
Ala Pro Ser Cys Ser Glu Lys Asp Gly Asn Tyr Ala Cys Leu Leu Arg
290 295 300
Glu Asp Gln Gly Trp Tyr Cys Lys Asn Ala Gly Ser Thr Val Tyr Tyr
305 310 315 320
Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325 330 335
Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Arg Glu Cys Asn Ile
340 345 350
Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355 360 365
Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370 375 380
Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385 390 395 400
Lys Gln Leu Pro Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
405 410 415
Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly
420 425 430
Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
435 440 445
Ile Arg Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
450 455 460
Glu Ser Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Lys Ile
465 470 475 480
Leu Asn Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
485 490 495
Leu Ile Ala Val Leu Gly Leu Thr Met Ile Ser Val Ser Ile Ile Ile
500 505 510
Ile Ile Lys Lys Thr Arg Lys Pro Thr Gly Ala Pro Pro Glu Leu Asn
515 520 525
Gly Val Thr Asn Gly Gly Phe Ile Pro His Ser
530 535

```

<210> 318
 <211> 1620
 <212> DNA
 <213> human metapneumo virus

<400> 318
 atgtcttgga aagtggatgattttttttca ttgttaataa cacctcaaca cggctcttaaa 60
 gagagctact tagaagagtc atgtagcact ataactgaag gatatactcag tgttctgagg 120
 acagggttggt acaccaatgt ttttacctg gaggtaggcg atgtagagaa cttacatgt 180
 gccgatggac ccagcttaat aaaaacagaa ttagacctga ccaaaagtgc actaagagag 240
 ctcaagaacag tttctgctga tcaactggca agagaggagc aaattgaaaa tcccagacaa 300
 tctagattcg ttctaggagc aatagcactc ggtgttgcaa ctgcagctgc agttacagca 360

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ggtgttgcaa ttgccaaaac catccggctt gaaagtgaag taacagcaat taagaatgcc 420
ctcaaaaaga ccaatgaagc agtatctaca ttggggaatg gagttcgtgt gttggcaact 480
gcagtgaagag agctgaaaga ttttgtgagc aagaatctaa cacgtgcaat caacaaaaac 540
aagtgcgaca ttgctgacct gaaaatggcc gtttagcttca gtcaattcaa cagaagggtc 600
ctaaatgttg tgcggcaatt ttcagacaac gctggaataa caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagagct gtttccaaca tgccaacatc tgcaggacaa 720
ataaaactga tgttgagaa ccgtgcaatg gtaagaagaa aagggttcgg aatcctgata 780
ggagtttacg gaagctccgt aatttacatg gtgcaactgc caatctttgg ggttatagac 840
acgcttgcgt ggatagtaaa agcagccctt tcttgttcag gaaaaaagg aaactatgct 900
tgctcttaa gagaagacca aggatggtat tgtcaaatg cagggtcaac tgtttactac 960
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tgcaaatgta gcacaggaag acatcctatc agtatggttg cactatctcc tcttggggct 1140
ttggttgctt gctacaaggg agtgagctgt tccattggca gcaacagagt agggatcatc 1200
aagcaactga acaaaggctg ctcttatata accaaccaag acgcagacac agtgacaata 1260
gacaacactg tataccagct aagcaaaagt gaaggcgaac agcatgttat aaaaggagg 1320
ccagtgtcaa gcagctttga cccagtcaag tttcctgaag atcaattcaa tgttgcaact 1380
gaccaagttt tcgagagcat tgagaacagt caggccttgg tggatcaatc aaacagaatc 1440
ctaagcagtg cagagaaaagg aaacactggc ttcacattg taataattct aattgctgtc 1500
cttggctcta ccatgatcct agtgagtgtt tttatcataa taaagaaaac aaagaaacc 1560
acaggagcac ctccagagct gagtgggtgc acaaacaatg gcttcatacc acataattag 1620

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<210> 319
<211> 1620
<212> DNA
<213> human metapneumo virus

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<400> 319
atgtcttgga aagtggatgat ctttttttca ttgctaataa caccctcaaca cggctcttaaa 60
gagagctacc tagaagaatc atgtagcact ataactgagg gatattcttag tgttctgagg 120
acaggttggg ataccaacgt ttttacatta gaggtgggtg atgtagaaaa ccttacatgt 180
tctgatggac ctagcctaata aaaaacagaa tttagatctga ccaaaagtgc actaagagag 240
ctcaaaacag tctctgctga ccaattggca agagaggaac aaattgagaa tccagacaa 300
tctaggtttg ttctaggagc aatagcactc ggtgttgcaa cagcagctgc agtcacagca 360
ggtgttgcaa ttgccaaaac catccggctt gagagtgaag tcacagcaat taagaatgcc 420
ctcaaaacga ccaatgaagc agtatctaca ttggggaatg gagttcgagt gttggcaact 480
gcagtgaagag agctaaaaga ctttgtgagc aagaatttaa ctctgtgcaat caacaaaaac 540
aagtgcgaca ttgatgacct aaaaatggct gttagcttca gtcaattcaa cagaagggtt 600
ctaaatgttg tgcggcaatt ttcagacaat gctggaataa caccagcaat atctttggac 660
ttaatgacag atgctgaact agccagggcc gtttctaaca tgccgacatc tgcaggacaa 720
ataaaattga tgttgagaa ccgtgcatg gtgcgaagaa aggggttcgg aatcctgata 780
ggggtctacg ggagctccgt aatttacacg gtgcagctgc caatctttgg cgttatagac 840
acgcttgcgt ggatagtaaa agcagccctt tcttgttcgg aaaaaaagg aaactatgct 900
tgctctttaa gagaagacca aggttggtat tgtcagaatg cagggtcaac tgtttactac 960
ccaaatgaga aagactgtga aacaagagga gacctgtct tttgcgacac agcagcagga 1020
attaatgttg ctgagcaatc aaaggagtgc aacatcaaca tatccactac aaattaccca 1080
tgcaaatgca gcacaggaag acatcctatc agtatggttg cactgtctcc tcttggggct 1140
ctggttgctt gctacaaagg agtaagctgt tccattggca gcaacagagt agggatcatc 1200
aagcagctga acaaagggtt ctcttatata accaaccaag atgcagacac agtgacaata 1260
gacaacactg tatatcagct aagcaaaagt gaggggtgaa agcatgttat aaaaggcaga 1320
ccagtgtcaa gcagctttga tccaatcaag tttcctgaag atcaattcaa tgttgcaact 1380
gaccaagttt ttgagaacat tgaaaacagc caggccttag tagatcaatc aaacagaatc 1440
ctaagcagtg cagagaaaagg gaatactggc tttatcattg taataattct aattgctgtc 1500
cttggctcta gcatgatcct agtgagcatc ttcattataa tcaagaaaac aaagaaacca 1560
acgggagcac ctccagagct gagtgggtgc acaaacaatg gcttcatacc acacagttag 1620

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<210> 320
<211> 1620
<212> DNA
<213> human metapneumo virus

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<400> 320

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atgtcttggg aagtgatgat catcatttctg ttactcataa caccacagca cgggctaaaag 60
gagagttatt tggaagaatc atgtagtact ataactgagg gatacctcag tgttttaaga 120
acaggctggg acactaatgt cttcacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctactttaat caaaacagaa cttgatctaa caaaaagtgc ttttaaggaa 240
ctcaaaacag tctctgctga tcagttggcg agagaggagc aaattgaaaa tcccagacaa 300
tcaagatttg tcttaggtgc gatagctctc ggagttgcta cagcagcagc agtcacagca 360
ggcattgcaa tagccaaaac cataaggctt gagagtgagg tgaatgcaat taaaggtgct 420
ctcaaaacaa ctaatgaagc agtatccaca ttaggggaatg gtgtgcgggt cctagccact 480
gcagtggag agctaaaaga atttgtgagc aaaaacctga ctagtgcatt caacaggaac 540
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattt 600
ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac 660
ctgatgactg atgctgagtt ggccagagct gtatcataca tgccaacatc tgcagggcag 720
ataaaaactg tgttgagaa ccgcgcaatg gtaaggagaa aaggatttgg aatcctgata 780
ggggtctacg gaagctctgt gatttacatg gtccaattgc cgtcttttgg tgtcatagat 840
acaccttggt ggatcatcaa ggcagctccc tcttgctcag aaaaaaacgg gaattatgct 900
tgctctctaa gagaggatca aggggtggtat tgtaaaaatg caggatctac tgtttactac 960
ccaaatgaaa aagactgcga aacaagaggt gatcatgttt tttgtgacac agcagcaggg 1020
atcaatgttg ctgagcaatc aagagaatgc aacatcaaca tatctactac caactaccca 1080
tgcaaagtca gcacaggaag acacctata agcatgggtg cactatcacc tctcgggtgct 1140
ttgggtggctt gctataaagg ggttaagctgc tctgattggc gcaattgggt tggaaatcatc 1200
aaacaattac ccaaaggctg ctcatacata accaaccagg atgcagacac tgtaacaatt 1260
gacaataccg tgtatcaact aagcaaaagt gaaggtgaac agcatgtaat aaaagggaga 1320
ccagtttcaa ccagttttga tccaatcaag tttcctgagg atcagttcaa tgttgcgctt 1380
gatcaagtct tcgaaagcat tgagaacagt caggcactag tggaccagtc aaacaaaatt 1440
ctaaacagtg cagaaaaagg aaacactggt ttcattatcg tagtaatttt ggttgctggt 1500
cttggtctaa ccatgatttc agtgagcacc atcatcataa tcaagaaaac aaggaagccc 1560
acaggagcac ctccagagct gaatggtgtc accaacggcg gtttcatacc acatagttag 1620

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<210> 321

<211> 1620

<212> DNA

<213> human metapneumo virus

<400> 321

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atgtcttggg aagtgatgat tatcatttctg ttactcataa cacctcagca cggactaaaa 60
gaaagttatt tagaagaatc atgtagtact ataactgaag gatattctcag tgttttaaga 120
acaggttggg acaccaatgt ctttacatta gaagttgggt atgttgaaaa tcttacatgt 180
actgatggac ctactttaat caaaacagaa cttgacctaa ccaaaagtgc tctgagagaa 240
ctcaaaacag tttctgctga tcagttagcg agagaagaac aaattgaaaa tcccagacaa 300
tcaaggtttg tcttaggtgc aatagctctt ggagttgcca cagcagcagc agtcacagca 360
ggcattgcaa tagccaaaac cataagactt ctaggaaatg gagtgcgagt cctagccact 480
ctcaaaacaa ccaacgaggg agtatccaca atttgtgagc aaaaacctga ctagtgcgat caacaagaac 540
gcagtaagag agctgaaaga atttgtgagc gtcagcttca gtcaattcaa cagaagattc 600
aaatgtgaca ttgctgatct gaagatggct gtcagcttca gtcaattcaa cagaagattc 660
ctaaatgttg tgcggcagtt ttcagacaat gcagggataa caccagcaat atcattggac 660
ctaatgactg atgctgagct ggccagagct gtatcataca tgccaacatc tgcaggacag 720
ataaaaacta tgttagagaa ccgtgcaatg gtgaggagaa aaggatttgg aatcctgata 780
ggggtctacg gaagctctgt gatttacatg gtccagctgc cgtcttttgg tgtcatagat 840
acaccttggt ggataatcaa ggcagctccc tcttgctcag aaaaagatgg aaattatgct 900
tgctctctaa gagaggatca aggggtggtat tgcaaaaatg caggatccac tgtttactac 960
ccaaatgaaa aagactgcga aacaagaggt gatcatgttt tttgtgacac agcagcaggg 1020
atcaatgttg ctgagcaatc aagagaatgc aacatcaaca tatctaccac caactaccca 1080
tgcaaaagtca gcacaggaag acacctatc agcatgggtg cactatcacc tctcgggtgct 1140
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gatcaagtct ttgaaagcat tgaaaacagt caagcactag tggaccagtc aaacaaaatt 1440
ctgaacagtg cagaaaaagg aaacactggt ttcattatcg taataatttt gattgctggt 1500
cttggtttaa ccatgatttc agtgagcacc atcatcataa tcaaaaaaac aaggaagccc 1560

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acagggggcac ctccagagct gaatgggtgtt accaacggcg gttttatacc gcatagtttag 1620

<210> 322
<211> 236
<212> PRT
<213> human metapneumo virus

<400> 322
Met Glu Val Lys Val Glu Asn Ile Arg Thr Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Val Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Lys Met Gln Lys Asn Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Ser Pro Met Glu Ser Ser Arg Glu Thr Pro Thr Val
65 70 75 80
Pro Thr Asp Asn Ser Asp Thr Asn Ser Ser Pro Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Gly Ser Thr Leu Tyr Phe Ala Ala Ser Ala Ser Ser
100 105 110
Pro Glu Thr Glu Pro Thr Ser Thr Pro Asp Thr Thr Asn Arg Pro Pro
115 120 125
Phe Val Asp Thr His Thr Thr Pro Pro Ser Ala Ser Arg Thr Lys Thr
130 135 140
Ser Pro Ala Val His Thr Lys Asn Asn Pro Arg Thr Ser Ser Arg Thr
145 150 155 160
His Ser Pro Pro Arg Ala Thr Thr Arg Thr Ala Arg Arg Thr Thr Thr
165 170 175
Leu Arg Thr Ser Ser Thr Arg Lys Arg Pro Ser Thr Ala Ser Val Gln
180 185 190
Pro Asp Ile Ser Ala Thr Thr His Lys Asn Glu Glu Ala Ser Pro Ala
195 200 205
Ser Pro Gln Thr Ser Ala Ser Thr Thr Arg Ile Gln Arg Lys Ser Val
210 215 220
Glu Ala Asn Thr Ser Thr Thr Tyr Asn Gln Thr Ser
225 230 235

<210> 323
<211> 219
<212> PRT
<213> human metapneumo virus

<400> 323
Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15
Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30
Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45
Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Thr Ser Glu Ser Glu His
50 55 60
His Thr Ser Ser Pro Pro Thr Glu Pro Asn Lys Glu Ala Ser Thr Ile
65 70 75 80
Ser Thr Asp Asn Pro Asp Ile Asn Pro Ser Ser Gln His Pro Thr Gln
85 90 95
Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Ala Ser Pro
100 105 110
Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser

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          115          120          125
Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
  130          135          140
Lys Pro Thr Val His Thr Ile Asn Asn Pro Asn Thr Ala Ser Ser Thr
  145          150          155          160
Gln Ser Pro Pro Arg Thr Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
          165          170          175
Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Leu Val Gln
          180          185          190
Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
          195          200          205
Asn Pro Gln Ala Ser Ala Ser Thr Met Gln Asn
  210          215

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<210> 324
 <211> 224
 <212> PRT
 <213> human metapneumo virus

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<400> 324
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1          5          10          15
Lys Ile Lys Asn Arg Ile Arg Ser Ser Arg Cys Tyr Arg Asn Ala Thr
          20          25          30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe
          35          40          45
Leu Ile Ile Asp His Ala Thr Leu Arg Asn Met Ile Lys Thr Glu Asn
          50          55          60
Cys Ala Asn Met Pro Ser Ala Glu Pro Ser Lys Lys Thr Pro Met Thr
          65          70          75          80
Ser Thr Ala Gly Pro Asn Thr Lys Pro Asn Pro Gln Gln Ala Thr Gln
          85          90          95
Trp Thr Thr Glu Asn Ser Thr Ser Pro Val Ala Thr Pro Glu Gly His
          100          105          110
Pro Tyr Thr Gly Thr Thr Gln Thr Ser Asp Thr Thr Ala Pro Gln Gln
          115          120          125
Thr Thr Asp Lys His Thr Ala Pro Leu Lys Ser Thr Asn Glu Gln Ile
          130          135          140
Thr Gln Thr Thr Thr Glu Lys Lys Thr Ile Arg Ala Thr Thr Gln Lys
          145          150          155          160
Arg Glu Lys Gly Lys Glu Asn Thr Asn Gln Thr Thr Ser Thr Ala Ala
          165          170          175
Thr Gln Thr Thr Asn Thr Thr Asn Gln Ile Arg Asn Ala Ser Glu Thr
          180          185          190
Ile Thr Thr Ser Asp Arg Pro Arg Thr Asp Thr Thr Thr Gln Ser Ser
          195          200          205
Glu Gln Thr Thr Arg Ala Thr Asp Pro Ser Ser Pro Pro His His Ala
          210          215          220

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<210> 325
 <211> 236
 <212> PRT
 <213> human metapneumo virus

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<400> 325
Met Glu Val Arg Val Glu Asn Ile Arg Ala Ile Asp Met Phe Lys Ala
  1          5          10          15
Lys Met Lys Asn Arg Ile Arg Ser Ser Lys Cys Tyr Arg Asn Ala Thr
          20          25          30
Leu Ile Leu Ile Gly Leu Thr Ala Leu Ser Met Ala Leu Asn Ile Phe

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<400>	327						
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cgtgtggcac	gtagcaaatg	ctttaaaaat	gcttctttaa	tctctatagg	aataactaca	120	
ctgagtatag	ctctcaatat	ctatctgtatc	ataaactaca	caatacaaaa	aaccactatc	180	
gaatcagaac	accacaccag	ctcaccaccc	acagaaccca	acaaggaagc	ttcaacaatc	240	
tccacagaca	accagacat	caatccaagc	tcacagcatc	caactcaaca	gtccacagaa	300	
aacccccac	tcaaccccg	agcatcagcg	agcccatcag	aaacagaacc	agcatcaaca	360	
ccagacacaa	caaaccgct	gtctccgta	gacaggtcca	cagcacaacc	aagtgaagc	420	
agaacaaaga	caaaaccgac	agtccacaca	atcaacaacc	caaacacagc	ttccagtaca	480	
caatccccac	cacggacaac	aacgaaggca	atccgcagag	ccaccacttt	ccgcatgagc	540	
aqcacaggaa	aaagaccaac	cacaacatta	gtccagtcgg	acagcagcac	cacaacccaa	600	

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aatcatgaag aaacaggttc agcgaaccca caggcgtctg caagcacaat gcaaaaactag 660

<210> 328
<211> 675
<212> DNA
<213> human metapneumo virus

<400> 328
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cgtataagaa gcagcaggtg ctatagaaat gctacactga tccttatttg actaacagcg 120
ttaagcatgg cacttaatat tttcctgac atcgatcatg caacattaag aaacatgac 180
aaaacagaaa actgtgctaa catgcccgtcg gcagaaccaa gcaaaaagac cccaatgacc 240
tccacagcag gcccaaacac caaacccaat ccacagcaag caacacagtg gaccacagag 300
aactcaacat cccacagtagc aaccccagag ggccatccat acacagggac aactcaaaaca 360
tcagacacaa cagctcccca gcaaaccaca gacaaacaca cagcaccgct aaaatcaacc 420
aatgaacaga tcaccagagc aaccacagag aaaaagacaa tcagagcaac aacccaaaaa 480
agggaaaaag gaaaagaaaa cacaaaccaa accacaagca cagctgcaac ccaaaacaacc 540
aacaccacca accaaatcag aaatgcaagt gagacaatca caacatccga cagaccaga 600
actgacacca caacccaaag cagcgaacag acaacccggg caacagaccc aagctcccca 660
ccacaccatg catag 675

<210> 329
<211> 711
<212> DNA
<213> human metapneumo virus

<400> 329
atggaagtaa gaggaggagaa cattcgggca atagacatgt tcaaagcaaa aatgaaaaac 60
cgtataagaa gtagcaagtg ctatagaaat gctacactga tccttatttg attaacagca 120
ttaagtatgg cacttaatat ttttttaatc attgattatg caatgtttaa aaacatgacc 180
aaagtggaa actgtgttaa tatgccgccg gtagaaccac gcaagaagac cccaatgacc 240
tctgcagtag acttaaacac caaacccaat ccacagcagg caacacagtt ggccgcagag 300
gattcaacat ctctagcagc aacctcagag gaccatctac acacagggac aactccaaca 360
ccagatgcaa cagtctctca gcaaaccaca gacgagtaca caacattgct gagatcaacc 420
aacagacaga ccacccaaac aaccacagag aaaaagccaa ccggagcaac aacccaaaaa 480
gaaaccacaa ctogaactac aagcacagct gcaacccaaa cactcaacac taccaaccaa 540
actagctatg tgagagagcg aaccacaaca tccgccagat ccagaaacag tgccacaact 600
caaagcagcg accaaacaac ccaggcagca gacccaagct cccaaccaca ccatacacag 660
aaaagcacaa caacaacata caacacagac acatcctctc caagtagtta a 711

<210> 330
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 330
Met Asp Pro Leu Asn Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
1 5 10 15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
20 25 30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
35 40 45
Ala Ile Glu Asn Pro Val Ile Glu His Val Arg Leu Lys Asn Ala Val
50 55 60
Asn Ser Lys Met Lys Ile Ser Asp Tyr Lys Ile Val Glu Pro Val Asn
65 70 75 80
Met Gln His Glu Ile Met Lys Asn Val His Ser Cys Glu Leu Thr Leu
85 90 95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Thr Leu Lys Leu
100 105 110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asp Thr

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115      120      125
Ser Ile Leu Ser Phe Ile Asp Val Glu Phe Ile Pro Ser Trp Val Ser
130      135      140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145      150      155      160
Arg Lys Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
165      170      175
Gly Lys Leu Val Phe Val Val Ser Ser Tyr Gly Cys Ile Val Lys Ser
180      185      190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
195      200      205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
210      215      220
Val Ser Asn Ser Leu Asn Glu Asn Gln Glu Gly Leu Gly Leu Arg Ser
225      230      235      240
Asn Leu Gln Gly Ile Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
245      250      255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
260      265      270
Glu Gly Phe Ile Met Ser Glu Ile Leu Arg Ile Thr Glu His Ala Gln
275      280      285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Asp Gln
290      295      300
Leu Thr Lys Leu Lys Asn Lys Asn Arg Leu Arg Val His Gly Thr Val
305      310      315      320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
325      330      335
Gly Asp Thr Leu Arg Cys Ile Lys Leu Ile Asn Lys Asn Leu Glu
340      345      350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
355      360      365
Val Asp Glu Arg Asp Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
370      375      380
Thr Lys Ile Leu Arg Trp Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385      390      395      400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
405      410      415
Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Thr Met Tyr Phe
420      425      430
Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Glu Gln Asp Phe
435      440      445
Leu Glu Leu Ala Ala Ile Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
450      455      460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465      470      475      480
Lys Arg Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Lys
485      490      495
Ile Lys Asn Arg Tyr Leu Glu Glu Thr Phe Asn Ala Ser Asp Ser Leu
500      505      510
Lys Thr Arg Arg Val Leu Glu Tyr Tyr Leu Lys Asp Asn Lys Phe Asp
515      520      525
Gln Lys Glu Leu Lys Ser Tyr Val Val Lys Gln Glu Tyr Leu Asn Asp
530      535      540
Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
545      550      555      560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
565      570      575
Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
580      585      590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
595      600      605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Arg Asn Asp Ser Tyr Asn

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610	615	620
Asn Tyr Ile Ala Arg	Ala Ser Ile Val Thr	Asp Leu Ser Lys Phe Asn
625	630	635
Gln Ala Phe Arg Tyr	Glu Thr Thr Ala Ile	Cys Ala Asp Val Ala Asp
645	650	655
Glu Leu His Gly Thr	Gln Ser Leu Phe Cys	Trp Leu His Leu Ile Val
660	665	670
Pro Met Thr Thr Met	Ile Cys Ala Tyr Arg	His Ala Pro Pro Glu Thr
675	680	685
Lys Gly Glu Tyr Asp	Ile Asp Lys Ile Glu	Glu Gln Ser Gly Leu Tyr
690	695	700
Arg Tyr His Met Gly	Gly Ile Glu Gly Trp	Cys Gln Lys Leu Trp Thr
705	710	715
Met Glu Ala Ile Ser	Leu Leu Asp Val Val	Ser Val Lys Thr Arg Cys
725	730	735
Gln Met Thr Ser Leu	Leu Asn Gly Asp	Asn Gln Ser Ile Asp Val Ser
740	745	750
Lys Pro Val Lys Leu	Ser Glu Gly Leu Asp	Glu Val Lys Ala Asp Tyr
755	760	765
Ser Leu Ala Val Lys	Met Leu Lys Glu Ile	Arg Asp Ala Tyr Arg Asn
770	775	780
Ile Gly His Lys Leu	Lys Glu Gly Glu Thr	Tyr Ile Ser Arg Asp Leu
785	790	795
Gln Phe Ile Ser Lys	Val Ile Gln Ser Glu	Gly Val Met His Pro Thr
805	810	815
Pro Ile Lys Lys Ile	Leu Arg Val Gly	Pro Trp Ile Asn Thr Ile Leu
820	825	830
Asp Asp Ile Lys Thr	Ser Ala Glu Ser Ile	Gly Ser Leu Cys Gln Glu
835	840	845
Leu Glu Phe Arg Gly	Glu Ser Ile Ile Val	Ser Leu Ile Leu Arg Asn
850	855	860
Phe Trp Leu Tyr Asn	Leu Tyr Met His Glu	Ser Lys Gln His Pro Leu
865	870	875
Ala Gly Lys Gln Leu	Phe Lys Gln Leu Asn	Lys Thr Leu Thr Ser Val
885	890	895
Gln Arg Phe Phe Glu	Ile Lys Lys Glu Asn	Glu Val Val Asp Leu Trp
900	905	910
Met Asn Ile Pro Met	Gln Phe Gly Gly Gly	Asp Pro Val Val Phe Tyr
915	920	925
Arg Ser Phe Tyr Arg	Arg Thr Pro Asp Phe	Leu Thr Glu Ala Ile Ser
930	935	940
His Val Asp Ile Leu	Leu Arg Ile Ser Ala	Asn Ile Arg Asn Glu Ala
945	950	955
Lys Ile Ser Phe Phe	Lys Ala Leu Leu Ser	Ile Glu Lys Asn Glu Arg
965	970	975
Ala Thr Leu Thr Thr	Leu Met Arg Asp	Pro Gln Ala Val Gly Ser Glu
980	985	990
Arg Gln Ala Lys Val	Thr Ser Asp Ile Asn	Arg Thr Ala Val Thr Ser
995	1000	1005
Ile Leu Ser Leu Ser	Pro Asn Gln Leu Phe	Ser Asp Ser Ala Ile His
1010	1015	1020
Tyr Ser Arg Asn Glu	Glu Glu Val Gly Ile	Ile Ala Asp Asn Ile Thr
1025	1030	1035
Pro Val Tyr Pro His	Gly Leu Arg Val Leu	Tyr Glu Ser Leu Pro Phe
1045	1050	1055
His Lys Ala Glu Lys	Val Val Asn Met Ile	Ser Gly Thr Lys Ser Ile
1060	1065	1070
Thr Asn Leu Leu Gln	Arg Thr Ser Ala Ile	Asn Gly Glu Asp Ile Asp
1075	1080	1085
Arg Ala Val Ser Met	Met Leu Glu Asn Leu	Gly Leu Leu Ser Arg Ile
1090	1095	1100
Leu Ser Val Val Val	Asp Ser Ile Glu Ile	Pro Thr Lys Ser Asn Gly

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1105          1110          1115          1120
Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Thr Ser Trp
          1125          1130          1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys
          1140          1145          1150
Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
          1155          1160          1165
Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys
          1170          1175          1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185          1190          1195          1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Arg Glu Gln Leu Glu Ala
          1205          1210          1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
          1220          1225          1230
Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys
          1235          1240          1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
          1250          1255          1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265          1270          1275          1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
          1285          1290          1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
          1300          1305          1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
          1315          1320          1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
          1330          1335          1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
1345          1350          1355          1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
          1365          1370          1375
Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
          1380          1385          1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
          1395          1400          1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
          1410          1415          1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp
1425          1430          1435          1440
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
          1445          1450          1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
          1460          1465          1470
Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu
          1475          1480          1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
          1490          1495          1500
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu
1505          1510          1515          1520
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
          1525          1530          1535
Arg Ser Ala Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly
          1540          1545          1550
Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
          1555          1560          1565
Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
          1570          1575          1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
1585          1590          1595          1600
Leu Leu Thr Pro Ile Pro Ser Pro Met Val Asn Leu Thr Gln Val Ile

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1605      1610      1615
Asp Pro Thr Glu Gln Leu Ala Tyr Phe Pro Lys Ile Thr Phe Glu Arg
1620      1625      1630
Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr
1635      1640      1645
Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
1650      1655      1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
1665      1670      1675      1680
Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
1685      1690      1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
1700      1705      1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
1715      1720      1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp
1730      1735      1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
1745      1750      1755      1760
His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr
1765      1770      1775
Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val
1780      1785      1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr
1795      1800      1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn
1810      1815      1820
Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
1825      1830      1835      1840
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
1845      1850      1855
His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
1860      1865      1870
Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn
1875      1880      1885
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
1890      1895      1900
Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Arg Arg Leu Leu Thr Leu
1905      1910      1915      1920
Gln Ser Asn His Ser Ser Val Ala Thr Val Gly Gly Ser Lys Val Ile
1925      1930      1935
Glu Ser Lys Trp Leu Thr Asn Lys Ala Asn Thr Ile Ile Asp Trp Leu
1940      1945      1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
1955      1960      1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
1970      1975      1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985      1990      1995      2000
Leu Val Ser Lys Lys
2005

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<210> 331
<211> 2005
<212> PRT
<213> human metapneumo virus

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<400> 331
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1      5      10      15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser

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                20                25                30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
      35      40      45
Ala Ile Glu Asn Pro Val Ile Glu His Val Arg Leu Lys Asn Ala Val
      50      55      60
Asn Ser Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
65      70      75      80
Met Gln His Glu Ile Met Lys Asn Val His Ser Cys Glu Leu Thr Leu
      85      90      95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Thr Leu Lys Leu
      100      105      110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asp Thr
      115      120      125
Ser Ile Leu Ser Phe Ile Asp Val Glu Phe Ile Pro Ser Trp Val Ser
      130      135      140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145      150      155      160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
      165      170      175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Ile Val Lys Ser
      180      185      190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
      195      200      205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
      210      215      220
Val Ser Asn Ser Leu Asn Glu Asn Gln Glu Gly Leu Gly Leu Arg Ser
225      230      235      240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
      245      250      255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
      260      265      270
Glu Gly Phe Ile Met Ser Glu Ile Leu Arg Ile Thr Glu His Ala Gln
      275      280      285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Asp Gln
      290      295      300
Leu Thr Lys Leu Lys Asn Lys Asn Arg Leu Arg Val His Gly Thr Val
305      310      315      320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
      325      330      335
Gly Asp Thr Leu Arg Cys Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
      340      345      350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
      355      360      365
Val Asp Glu Arg Asp Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
      370      375      380
Thr Lys Ile Leu Arg Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385      390      395      400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
      405      410      415
Lys Ile Lys Asn Leu Ile Val Leu Ser Lys Arg Trp Thr Met Tyr Phe
      420      425      430
Lys Ala Lys Asn Tyr Pro Ser Gln Leu Glu Leu Ser Glu Gln Asp Phe
      435      440      445
Leu Glu Leu Ala Ala Ile Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
      450      455      460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465      470      475      480
Lys Arg Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr
      485      490      495
Ile Lys Asn Arg Tyr Leu Glu Glu Thr Phe Asn Ala Ser Asp Ser Leu
      500      505      510
Lys Thr Arg Arg Val Leu Glu Tyr Tyr Leu Lys Asp Asn Lys Phe Asp

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515					520					525					
Gln	Lys	Glu	Leu	Lys	Ser	Tyr	Val	Val	Arg	Gln	Glu	Tyr	Leu	Asn	Asp
530						535				540					
Lys	Glu	His	Ile	Val	Ser	Leu	Thr	Gly	Lys	Glu	Arg	Glu	Leu	Ser	Val
545					550					555					560
Gly	Arg	Met	Phe	Ala	Met	Gln	Pro	Gly	Lys	Gln	Arg	Gln	Ile	Gln	Ile
				565					570					575	
Leu	Ala	Glu	Lys	Leu	Leu	Ala	Asp	Asn	Ile	Val	Pro	Phe	Phe	Pro	Glu
			580					585					590		
Thr	Leu	Thr	Lys	Tyr	Gly	Asp	Leu	Asp	Leu	Gln	Arg	Ile	Met	Glu	Ile
		595				600						605			
Lys	Ser	Glu	Leu	Ser	Ser	Ile	Lys	Thr	Arg	Arg	Asn	Asp	Ser	Tyr	Asn
610						615					620				
Asn	Tyr	Ile	Ala	Arg	Ala	Ser	Ile	Val	Thr	Asp	Leu	Ser	Lys	Phe	Asn
625					630					635					640
Gln	Ala	Phe	Arg	Tyr	Glu	Thr	Thr	Ala	Ile	Cys	Ala	Asp	Val	Ala	Asp
				645					650					655	
Glu	Leu	His	Gly	Thr	Gln	Ser	Leu	Phe	Cys	Trp	Leu	His	Leu	Ile	Val
			660					665					670		
Pro	Met	Thr	Thr	Met	Ile	Cys	Ala	Tyr	Arg	His	Ala	Pro	Pro	Glu	Thr
		675				680						685			
Lys	Gly	Glu	Tyr	Asp	Ile	Asp	Lys	Ile	Glu	Glu	Gln	Ser	Gly	Leu	Tyr
690						695					700				
Arg	Tyr	His	Met	Gly	Gly	Ile	Glu	Gly	Trp	Cys	Gln	Lys	Leu	Trp	Thr
705					710					715					720
Met	Glu	Ala	Ile	Ser	Leu	Leu	Asp	Val	Val	Ser	Val	Lys	Thr	Arg	Cys
				725					730					735	
Gln	Met	Thr	Ser	Leu	Leu	Asn	Gly	Asp	Asn	Gln	Ser	Ile	Asp	Val	Ser
			740				745						750		
Lys	Pro	Val	Lys	Leu	Ser	Glu	Gly	Leu	Asp	Glu	Val	Lys	Ala	Asp	Tyr
		755				760						765			
Arg	Leu	Ala	Ile	Lys	Met	Leu	Lys	Glu	Ile	Arg	Asp	Ala	Tyr	Arg	Asn
770						775					780				
Ile	Gly	His	Lys	Leu	Lys	Glu	Gly	Glu	Thr	Tyr	Ile	Ser	Arg	Asp	Leu
785					790					795					800
Gln	Phe	Ile	Ser	Lys	Val	Ile	Gln	Ser	Glu	Gly	Val	Met	His	Pro	Thr
				805					810					815	
Pro	Ile	Lys	Lys	Val	Leu	Arg	Val	Gly	Pro	Trp	Ile	Asn	Thr	Ile	Leu
			820					825					830		
Asp	Asp	Ile	Lys	Thr	Ser	Ala	Glu	Ser	Ile	Gly	Ser	Leu	Cys	Gln	Glu
		835					840					845			
Leu	Glu	Phe	Arg	Gly	Glu	Ser	Ile	Ile	Val	Ser	Leu	Ile	Leu	Arg	Asn
		850				855					860				
Phe	Trp	Leu	Tyr	Asn	Leu	Tyr	Met	His	Glu	Ser	Lys	Gln	His	Pro	Leu
865					870					875					880
Ala	Gly	Lys	Gln	Leu	Phe	Lys	Gln	Leu	Asn	Lys	Thr	Leu	Thr	Ser	Val
				885					890					895	
Gln	Arg	Phe	Phe	Glu	Ile	Lys	Lys	Glu	Asn	Glu	Val	Val	Asp	Leu	Trp
		900						905					910		
Met	Asn	Ile	Pro	Met	Gln	Phe	Gly	Gly	Gly	Asp	Pro	Val	Val	Phe	Tyr
		915					920					925			
Arg	Ser	Phe	Tyr	Arg	Arg	Thr	Pro	Asp	Phe	Leu	Thr	Glu	Ala	Ile	Ser
		930				935					940				
His	Val	Asp	Ile	Leu	Leu	Lys	Ile	Ser	Ala	Asn	Ile	Lys	Asn	Glu	Thr
945					950					955					960
Lys	Val	Ser	Phe	Phe	Lys	Ala	Leu	Leu	Ser	Ile	Glu	Lys	Asn	Glu	Arg
				965					970					975	
Ala	Thr	Leu	Thr	Thr	Leu	Met	Arg	Asp	Pro	Gln	Ala	Val	Gly	Ser	Glu
			980					985					990		
Arg	Gln	Ala	Lys	Val	Thr	Ser	Asp	Ile	Asn	Arg	Thr	Ala	Val	Thr	Ser
			995				1000					1005			
Ile	Leu	Ser	Leu	Ser	Pro	Asn	Gln	Leu	Phe	Ser	Asp	Ser	Ala	Ile	His

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1010          1015          1020
Tyr Ser Arg Asn Glu Glu Val Gly Ile Ile Ala Glu Asn Ile Thr
1025          1030          1035          1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
          1045          1050          1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
          1060          1065          1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
          1075          1080          1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
          1090          1095          1100
Leu Ser Val Val Val Asp Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
1105          1110          1115          1120
Arg Leu Ile Cys Cys Gln Ile Ser Arg Thr Leu Arg Glu Thr Ser Trp
          1125          1130          1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Thr Thr Cys
          1140          1145          1150
Met Asp Val Ile Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
          1155          1160          1165
Glu Lys Phe Ser Thr Asp Arg Thr Thr Arg Gly Gln Arg Gly Pro Lys
          1170          1175          1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185          1190          1195          1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Arg Glu Gln Leu Glu Ala
          1205          1210          1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
          1220          1225          1230
Leu Leu Asn Lys Ile Cys Leu Gly Ser Leu Gly Ile Ser Tyr Lys Cys
          1235          1240          1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
          1250          1255          1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265          1270          1275          1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
          1285          1290          1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
          1300          1305          1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
          1315          1320          1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
          1330          1335          1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
1345          1350          1355          1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
          1365          1370          1375
Asp Met Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
          1380          1385          1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
          1395          1400          1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly
          1410          1415          1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Lys Lys Asp Trp
1425          1430          1435          1440
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe
          1445          1450          1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly
          1460          1465          1470
Lys Asn Ile Lys Asp Glu Asp Ile Val Asp Glu Ser Ile Asp Lys Leu
          1475          1480          1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe
          1490          1495          1500
Glu Pro Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu

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1505          1510          1515          1520
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu
          1525          1530          1535
Arg Ser Ala Glu Leu His Glu Ile Pro Trp Ile Val Asn Ala Glu Gly
          1540          1545          1550
Asp Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu
          1555          1560          1565
Gln Ser Leu Phe Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala
          1570          1575          1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala
1585          1590          1595          1600
Leu Leu Thr Pro Ile Ser Ser Pro Met Val Asn Leu Thr Gln Val Ile
          1605          1610          1615
Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Lys Ile Thr Phe Glu Arg
          1620          1625          1630
Leu Lys Asn Tyr Asp Thr Ser Ser Asn Tyr Ala Lys Gly Lys Leu Thr
          1635          1640          1645
Arg Asn Tyr Met Ile Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn
          1650          1655          1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile
1665          1670          1675          1680
Gly Lys Leu Met Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly
          1685          1690          1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp
          1700          1705          1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr
          1715          1720          1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Glu Leu Ser Arg Ile Ile Asp
          1730          1735          1740
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr
1745          1750          1755          1760
His Trp Asp Leu Ile His Arg Val Ser Lys Asp Ala Leu Leu Ile Thr
          1765          1770          1775
Leu Cys Asp Ala Glu Phe Lys Asp Arg Asp Asp Phe Phe Lys Met Val
          1780          1785          1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Thr Tyr
          1795          1800          1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Lys Asp Cys Asn
          1810          1815          1820
Val Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln
1825          1830          1835          1840
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly
          1845          1850          1855
His His Asn Ser Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met
          1860          1865          1870
Lys Ile Ala Val Cys Asn Asp Phe Tyr Ala Ala Lys Lys Leu Asp Asn
          1875          1880          1885
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile
          1890          1895          1900
Pro Ile Asn Lys Lys Glu Leu Asp Arg Gln Arg Arg Leu Leu Thr Leu
1905          1910          1915          1920
Gln Ser Asn His Ser Ser Val Ala Thr Val Gly Gly Ser Lys Ile Ile
          1925          1930          1935
Glu Ser Lys Trp Leu Thr Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
          1940          1945          1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
          1955          1960          1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
          1970          1975          1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985          1990          1995          2000
Leu Val Ser Lys Lys

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2005

<210> 332
<211> 2005
<212> PRT
<213> human metapneumo virus

<400> 332
Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
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Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
20 25 30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Asn Asp Asn Thr Ala Lys Val
35 40 45
Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
50 55 60
Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Val Asn
65 70 75 80
Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
85 90 95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
100 105 110
Asn Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
115 120 125
Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
130 135 140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145 150 155 160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
165 170 175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
180 185 190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
195 200 205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
210 215 220
Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Leu Arg Ser
225 230 235 240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
245 250 255
Met Leu Ser Leu Cys Cys Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
260 265 270
Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
275 280 285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
290 295 300
Leu Ser Val Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
305 310 315 320
Leu Glu Asn Asn Asn Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu
325 330 335
Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
340 345 350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
355 360 365
Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
370 375 380
Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385 390 395 400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
405 410 415
Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Ala Met Tyr Phe

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          420          425          430
Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
          435          440          445
Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
          450          455          460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465          470          475          480
Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Thr
          485          490          495
Ile Lys Asn Gln Tyr Leu Glu Glu Ala Phe Asn Ala Ser Asp Ser Gln
          500          505          510
Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
          515          520          525
Gln Lys Glu Leu Lys Arg Tyr Val Ile Lys Gln Glu Tyr Leu Asn Asp
          530          535          540
Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
545          550          555          560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
          565          570          575
Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
          580          585          590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Ile
          595          600          605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
          610          615          620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
625          630          635          640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
          645          650          655
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
          660          665          670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
          675          680          685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Gln Glu Gln Ser Gly Leu Tyr
          690          695          700
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
705          710          715          720
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
          725          730          735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
          740          745          750
Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
          755          760          765
Ser Leu Ala Ile Arg Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
          770          775          780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785          790          795          800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
          805          810          815
Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu
          820          825          830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
          835          840          845
Leu Glu Phe Arg Gly Glu Ser Ile Leu Val Ser Leu Ile Leu Arg Asn
          850          855          860
Phe Trp Leu Tyr Asn Leu Tyr Met Tyr Glu Ser Lys Gln His Pro Leu
865          870          875          880
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
          885          890          895
Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
          900          905          910
Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr

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          915          920          925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
 930          935          940
His Val Asp Leu Leu Leu Lys Val Ser Asn Asn Ile Lys Asp Glu Thr
 945          950          955          960
Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
          965          970          975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
          980          985          990
Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
          995          1000          1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Cys Asp Ser Ala Ile His
 1010          1015          1020
Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
 1025          1030          1035          1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
          1045          1050          1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
          1060          1065          1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
          1075          1080          1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
 1090          1095          1100
Leu Ser Val Ile Ile Asn Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
 1105          1110          1115          1120
Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
          1125          1130          1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Val Thr Cys
          1140          1145          1150
Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
          1155          1160          1165
Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
 1170          1175          1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
 1185          1190          1195          1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
          1205          1210          1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
          1220          1225          1230
Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
          1235          1240          1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
          1250          1255          1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
 1265          1270          1275          1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
          1285          1290          1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
          1300          1305          1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr
          1315          1320          1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile
          1330          1335          1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu
 1345          1350          1355          1360
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile
          1365          1370          1375
Asp Ile Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln
          1380          1385          1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn
          1395          1400          1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly

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1410	1415	1420
Ile Leu Thr Glu Gln Cys Ile Glu Asn Asn Ile Phe Arg Lys Asp Trp		
1425	1430	1435
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Val Phe		1440
	1445	1450
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly		1455
	1460	1465
Lys Asn Val Lys Asp Glu Asp Ile Ile Asp Glu Ser Ile Asp Lys Leu		1470
	1475	1480
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe		1485
	1490	1495
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu		1500
1505	1510	1515
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu		1520
	1525	1530
Arg Val Val Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly		1535
	1540	1545
Glu Leu Val Glu Ile Lys Ser Ile Lys Ile Tyr Leu Gln Leu Ile Glu		1550
	1555	1560
Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala		1565
	1570	1575
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala		1580
1585	1590	1595
Leu Phe Asn Pro Ser Ser Ser Pro Met Phe Asn Leu Thr Gln Val Ile		1600
	1605	1610
Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Arg Ile Ile Phe Glu Arg		1615
	1620	1625
Leu Lys Ser Tyr Asp Thr Ser Ser Asp Tyr Asn Lys Gly Lys Leu Thr		1630
	1635	1640
Arg Asn Tyr Met Thr Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn		1645
	1650	1655
Phe Val Phe Ser Ser Thr Gly Cys Lys Val Ser Leu Lys Thr Cys Ile		1660
1665	1670	1675
Gly Lys Leu Ile Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly		1680
	1685	1690
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp		1695
	1700	1705
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr		1710
	1715	1720
Pro Leu Glu Tyr Gln Arg Val Ile Gly Asp Leu Asn Arg Val Ile Asp		1725
	1730	1735
Ser Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr		1740
1745	1750	1755
His Trp Asp Leu Ile His Arg Ile Ser Lys Asp Ala Leu Leu Ile Thr		1760
	1765	1770
Leu Cys Asp Ala Glu Phe Lys Asn Arg Asp Asp Phe Phe Lys Met Val		1775
	1780	1785
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Ala Tyr		1790
	1795	1800
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Val Asp Cys Asn		1805
	1810	1815
Ile Lys Leu Pro Phe Phe Val Arg Ser Val Ala Thr Phe Ile Met Gln		1820
1825	1830	1835
Gly Ser Lys Leu Ser Gly Ser Glu Cys Tyr Ile Leu Leu Thr Leu Gly		1840
	1845	1850
His His Asn Asn Leu Pro Cys His Gly Glu Ile Gln Asn Ser Lys Met		1855
	1860	1865
Arg Ile Ala Val Cys Asn Asp Phe Tyr Ala Ser Lys Lys Leu Asp Asn		1870
	1875	1880
Lys Ser Ile Glu Ala Asn Cys Lys Ser Leu Leu Ser Gly Leu Arg Ile		1885
	1890	1895
Pro Ile Asn Lys Lys Glu Leu Asn Arg Gln Lys Lys Leu Leu Thr Leu		1900

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1905          1910          1915          1920
Gln Ser Asn His Ser Ser Ile Ala Thr Val Gly Gly Ser Lys Ile Ile
          1925          1930          1935
Glu Ser Lys Trp Leu Lys Asn Lys Ala Ser Thr Ile Ile Asp Trp Leu
          1940          1945          1950
Glu His Ile Leu Asn Ser Pro Lys Gly Glu Leu Asn Tyr Asp Phe Phe
          1955          1960          1965
Glu Ala Leu Glu Asn Thr Tyr Pro Asn Met Ile Lys Leu Ile Asp Asn
          1970          1975          1980
Leu Gly Asn Ala Glu Ile Lys Lys Leu Ile Lys Val Thr Gly Tyr Met
1985          1990          1995          2000
Leu Val Ser Lys Lys
          2005

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<210> 333
<211> 2005
<212> PRT
<213> human metapneumo virus

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<400> 333
Met Asp Pro Phe Cys Glu Ser Thr Val Asn Val Tyr Leu Pro Asp Ser
 1      5      10      15
Tyr Leu Lys Gly Val Ile Ser Phe Ser Glu Thr Asn Ala Ile Gly Ser
 20     25     30
Cys Leu Leu Lys Arg Pro Tyr Leu Lys Lys Asp Asn Thr Ala Lys Val
 35     40     45
Ala Val Glu Asn Pro Val Val Glu His Val Arg Leu Arg Asn Ala Val
 50     55     60
Met Thr Lys Met Lys Ile Ser Asp Tyr Lys Val Val Glu Pro Ile Asn
 65     70     75     80
Met Gln His Glu Ile Met Lys Asn Ile His Ser Cys Glu Leu Thr Leu
 85     90     95
Leu Lys Gln Phe Leu Thr Arg Ser Lys Asn Ile Ser Ser Leu Lys Leu
100    105    110
Ser Met Ile Cys Asp Trp Leu Gln Leu Lys Ser Thr Ser Asp Asn Thr
115    120    125
Ser Ile Leu Asn Phe Ile Asp Val Glu Phe Ile Pro Val Trp Val Ser
130    135    140
Asn Trp Phe Ser Asn Trp Tyr Asn Leu Asn Lys Leu Ile Leu Glu Phe
145    150    155    160
Arg Arg Glu Glu Val Ile Arg Thr Gly Ser Ile Leu Cys Arg Ser Leu
165    170    175
Gly Lys Leu Val Phe Ile Val Ser Ser Tyr Gly Cys Val Val Lys Ser
180    185    190
Asn Lys Ser Lys Arg Val Ser Phe Phe Thr Tyr Asn Gln Leu Leu Thr
195    200    205
Trp Lys Asp Val Met Leu Ser Arg Phe Asn Ala Asn Phe Cys Ile Trp
210    215    220
Val Ser Asn Asn Leu Asn Lys Asn Gln Glu Gly Leu Gly Phe Arg Ser
225    230    235    240
Asn Leu Gln Gly Met Leu Thr Asn Lys Leu Tyr Glu Thr Val Asp Tyr
245    250    255
Met Leu Ser Leu Cys Ser Asn Glu Gly Phe Ser Leu Val Lys Glu Phe
260    265    270
Glu Gly Phe Ile Met Ser Glu Ile Leu Lys Ile Thr Glu His Ala Gln
275    280    285
Phe Ser Thr Arg Phe Arg Asn Thr Leu Leu Asn Gly Leu Thr Glu Gln
290    295    300
Leu Ser Met Leu Lys Ala Lys Asn Arg Ser Arg Val Leu Gly Thr Ile
305    310    315    320
Leu Glu Asn Asn Asp Tyr Pro Met Tyr Glu Val Val Leu Lys Leu Leu

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          325          330          335
Gly Asp Thr Leu Lys Ser Ile Lys Leu Leu Ile Asn Lys Asn Leu Glu
          340          345          350
Asn Ala Ala Glu Leu Tyr Tyr Ile Phe Arg Ile Phe Gly His Pro Met
          355          360          365
Val Asp Glu Arg Glu Ala Met Asp Ala Val Lys Leu Asn Asn Glu Ile
          370          375          380
Thr Lys Ile Leu Lys Leu Glu Ser Leu Thr Glu Leu Arg Gly Ala Phe
385          390          395          400
Ile Leu Arg Ile Ile Lys Gly Phe Val Asp Asn Asn Lys Arg Trp Pro
          405          410          415
Lys Ile Lys Asn Leu Lys Val Leu Ser Lys Arg Trp Val Met Tyr Phe
          420          425          430
Lys Ala Lys Ser Tyr Pro Ser Gln Leu Glu Leu Ser Val Gln Asp Phe
          435          440          445
Leu Glu Leu Ala Ala Val Gln Phe Glu Gln Glu Phe Ser Val Pro Glu
450          455          460
Lys Thr Asn Leu Glu Met Val Leu Asn Asp Lys Ala Ile Ser Pro Pro
465          470          475          480
Lys Lys Leu Ile Trp Ser Val Tyr Pro Lys Asn Tyr Leu Pro Glu Ile
          485          490          495
Ile Lys Asn Gln Tyr Leu Glu Glu Val Phe Asn Ala Ser Asp Ser Gln
          500          505          510
Arg Thr Arg Arg Val Leu Glu Phe Tyr Leu Lys Asp Cys Lys Phe Asp
          515          520          525
Gln Lys Asp Leu Lys Arg Tyr Val Leu Lys Gln Glu Tyr Leu Asn Asp
          530          535          540
Lys Asp His Ile Val Ser Leu Thr Gly Lys Glu Arg Glu Leu Ser Val
545          550          555          560
Gly Arg Met Phe Ala Met Gln Pro Gly Lys Gln Arg Gln Ile Gln Ile
          565          570          575
Leu Ala Glu Lys Leu Leu Ala Asp Asn Ile Val Pro Phe Phe Pro Glu
          580          585          590
Thr Leu Thr Lys Tyr Gly Asp Leu Asp Leu Gln Arg Ile Met Glu Met
          595          600          605
Lys Ser Glu Leu Ser Ser Ile Lys Thr Arg Lys Asn Asp Ser Tyr Asn
          610          615          620
Asn Tyr Ile Ala Arg Ala Ser Ile Val Thr Asp Leu Ser Lys Phe Asn
625          630          635          640
Gln Ala Phe Arg Tyr Glu Thr Thr Ala Ile Cys Ala Asp Val Ala Asp
          645          650          655
Glu Leu His Gly Thr Gln Ser Leu Phe Cys Trp Leu His Leu Ile Val
          660          665          670
Pro Met Thr Thr Met Ile Cys Ala Tyr Arg His Ala Pro Pro Glu Thr
          675          680          685
Lys Gly Glu Tyr Asp Ile Asp Lys Ile Glu Glu Gln Ser Gly Leu Tyr
          690          695          700
Arg Tyr His Met Gly Gly Ile Glu Gly Trp Cys Gln Lys Leu Trp Thr
705          710          715          720
Met Glu Ala Ile Ser Leu Leu Asp Val Val Ser Val Lys Thr Arg Cys
          725          730          735
Gln Met Thr Ser Leu Leu Asn Gly Asp Asn Gln Ser Ile Asp Val Ser
          740          745          750
Lys Pro Val Lys Leu Ser Glu Gly Ile Asp Glu Val Lys Ala Asp Tyr
          755          760          765
Ser Leu Ala Ile Lys Met Leu Lys Glu Ile Arg Asp Ala Tyr Lys Asn
          770          775          780
Ile Gly His Lys Leu Lys Glu Gly Glu Thr Tyr Ile Ser Arg Asp Leu
785          790          795          800
Gln Phe Ile Ser Lys Val Ile Gln Ser Glu Gly Val Met His Pro Thr
          805          810          815
Pro Ile Lys Lys Ile Leu Arg Val Gly Pro Trp Ile Asn Thr Ile Leu

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      820      825      830
Asp Asp Ile Lys Thr Ser Ala Glu Ser Ile Gly Ser Leu Cys Gln Glu
      835      840      845
Leu Glu Phe Arg Gly Glu Ser Met Leu Val Ser Leu Ile Leu Arg Asn
      850      855      860
Phe Trp Leu Tyr Asn Leu Tyr Met His Glu Ser Lys Gln His Pro Leu
865      870      875      880
Ala Gly Lys Gln Leu Phe Lys Gln Leu Asn Lys Thr Leu Thr Ser Val
      885      890      895
Gln Arg Phe Phe Glu Leu Lys Lys Glu Asn Asp Val Val Asp Leu Trp
      900      905      910
Met Asn Ile Pro Met Gln Phe Gly Gly Gly Asp Pro Val Val Phe Tyr
      915      920      925
Arg Ser Phe Tyr Arg Arg Thr Pro Asp Phe Leu Thr Glu Ala Ile Ser
      930      935      940
His Val Asp Leu Leu Leu Lys Val Ser Asn Asn Ile Lys Asn Glu Thr
945      950      955      960
Lys Ile Arg Phe Phe Lys Ala Leu Leu Ser Ile Glu Lys Asn Glu Arg
      965      970      975
Ala Thr Leu Thr Thr Leu Met Arg Asp Pro Gln Ala Val Gly Ser Glu
      980      985      990
Arg Gln Ala Lys Val Thr Ser Asp Ile Asn Arg Thr Ala Val Thr Ser
      995      1000      1005
Ile Leu Ser Leu Ser Pro Asn Gln Leu Phe Cys Asp Ser Ala Ile His
      1010      1015      1020
Tyr Ser Arg Asn Glu Glu Glu Val Gly Ile Ile Ala Asp Asn Ile Thr
1025      1030      1035      1040
Pro Val Tyr Pro His Gly Leu Arg Val Leu Tyr Glu Ser Leu Pro Phe
      1045      1050      1055
His Lys Ala Glu Lys Val Val Asn Met Ile Ser Gly Thr Lys Ser Ile
      1060      1065      1070
Thr Asn Leu Leu Gln Arg Thr Ser Ala Ile Asn Gly Glu Asp Ile Asp
      1075      1080      1085
Arg Ala Val Ser Met Met Leu Glu Asn Leu Gly Leu Leu Ser Arg Ile
      1090      1095      1100
Leu Ser Val Ile Ile Asn Ser Ile Glu Ile Pro Ile Lys Ser Asn Gly
1105      1110      1115      1120
Arg Leu Ile Cys Cys Gln Ile Ser Lys Thr Leu Arg Glu Lys Ser Trp
      1125      1130      1135
Asn Asn Met Glu Ile Val Gly Val Thr Ser Pro Ser Ile Val Thr Cys
      1140      1145      1150
Met Asp Val Val Tyr Ala Thr Ser Ser His Leu Lys Gly Ile Ile Ile
      1155      1160      1165
Glu Lys Phe Ser Thr Asp Lys Thr Thr Arg Gly Gln Arg Gly Pro Lys
      1170      1175      1180
Ser Pro Trp Val Gly Ser Ser Thr Gln Glu Lys Lys Leu Val Pro Val
1185      1190      1195      1200
Tyr Asn Arg Gln Ile Leu Ser Lys Gln Gln Lys Glu Gln Leu Glu Ala
      1205      1210      1215
Ile Gly Lys Met Arg Trp Val Tyr Lys Gly Thr Pro Gly Leu Arg Arg
      1220      1225      1230
Leu Leu Asn Lys Ile Cys Ile Gly Ser Leu Gly Ile Ser Tyr Lys Cys
      1235      1240      1245
Val Lys Pro Leu Leu Pro Arg Phe Met Ser Val Asn Phe Leu His Arg
      1250      1255      1260
Leu Ser Val Ser Ser Arg Pro Met Glu Phe Pro Ala Ser Val Pro Ala
1265      1270      1275      1280
Tyr Arg Thr Thr Asn Tyr His Phe Asp Thr Ser Pro Ile Asn Gln Ala
      1285      1290      1295
Leu Ser Glu Arg Phe Gly Asn Glu Asp Ile Asn Leu Val Phe Gln Asn
      1300      1305      1310
Ala Ile Ser Cys Gly Ile Ser Ile Met Ser Val Val Glu Gln Leu Thr

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1315	1320	1325
Gly Arg Ser Pro Lys Gln Leu Val Leu Ile Pro Gln Leu Glu Glu Ile		
1330	1335	1340
Asp Ile Met Pro Pro Pro Val Phe Gln Gly Lys Phe Asn Tyr Lys Leu		
1345	1350	1355
Val Asp Lys Ile Thr Ser Asp Gln His Ile Phe Ser Pro Asp Lys Ile		
1365	1370	1375
Asp Ile Leu Thr Leu Gly Lys Met Leu Met Pro Thr Ile Lys Gly Gln		
1380	1385	1390
Lys Thr Asp Gln Phe Leu Asn Lys Arg Glu Asn Tyr Phe His Gly Asn		
1395	1400	1405
Asn Leu Ile Glu Ser Leu Ser Ala Ala Leu Ala Cys His Trp Cys Gly		
1410	1415	1420
Ile Leu Thr Glu Gln Cys Val Glu Asn Asn Ile Phe Arg Lys Asp Trp		
1425	1430	1435
Gly Asp Gly Phe Ile Ser Asp His Ala Phe Met Asp Phe Lys Ile Phe		
1445	1450	1455
Leu Cys Val Phe Lys Thr Lys Leu Leu Cys Ser Trp Gly Ser Gln Gly		
1460	1465	1470
Lys Asn Val Lys Asp Glu Asp Ile Ile Asp Glu Ser Ile Asp Lys Leu		
1475	1480	1485
Leu Arg Ile Asp Asn Thr Phe Trp Arg Met Phe Ser Lys Val Met Phe		
1490	1495	1500
Glu Ser Lys Val Lys Lys Arg Ile Met Leu Tyr Asp Val Lys Phe Leu		
1505	1510	1515
Ser Leu Val Gly Tyr Ile Gly Phe Lys Asn Trp Phe Ile Glu Gln Leu		
1525	1530	1535
Arg Val Val Glu Leu His Glu Val Pro Trp Ile Val Asn Ala Glu Gly		
1540	1545	1550
Glu Leu Val Glu Ile Lys Pro Ile Lys Ile Tyr Leu Gln Leu Ile Glu		
1555	1560	1565
Gln Ser Leu Ser Leu Arg Ile Thr Val Leu Asn Tyr Thr Asp Met Ala		
1570	1575	1580
His Ala Leu Thr Arg Leu Ile Arg Lys Lys Leu Met Cys Asp Asn Ala		
1585	1590	1595
Leu Phe Asn Pro Ser Ser Ser Pro Met Phe Ser Leu Thr Gln Val Ile		
1605	1610	1615
Asp Pro Thr Thr Gln Leu Asp Tyr Phe Pro Lys Val Ile Phe Glu Arg		
1620	1625	1630
Leu Lys Ser Tyr Asp Thr Ser Ser Asp Tyr Asn Lys Gly Lys Leu Thr		
1635	1640	1645
Arg Asn Tyr Met Thr Leu Leu Pro Trp Gln His Val Asn Arg Tyr Asn		
1650	1655	1660
Phe Val Phe Ser Ser Thr Gly Cys Lys Ile Ser Leu Lys Thr Cys Ile		
1665	1670	1675
Gly Lys Leu Ile Lys Asp Leu Asn Pro Lys Val Leu Tyr Phe Ile Gly		
1685	1690	1695
Glu Gly Ala Gly Asn Trp Met Ala Arg Thr Ala Cys Glu Tyr Pro Asp		
1700	1705	1710
Ile Lys Phe Val Tyr Arg Ser Leu Lys Asp Asp Leu Asp His His Tyr		
1715	1720	1725
Pro Leu Glu Tyr Gln Arg Val Ile Gly Asp Leu Asn Arg Val Ile Asp		
1730	1735	1740
Gly Gly Glu Gly Leu Ser Met Glu Thr Thr Asp Ala Thr Gln Lys Thr		
1745	1750	1755
His Trp Asp Leu Ile His Arg Ile Ser Lys Asp Ala Leu Leu Ile Thr		
1765	1770	1775
Leu Cys Asp Ala Glu Phe Lys Asn Arg Asp Asp Phe Phe Lys Met Val		
1780	1785	1790
Ile Leu Trp Arg Lys His Val Leu Ser Cys Arg Ile Cys Thr Ala Tyr		
1795	1800	1805
Gly Thr Asp Leu Tyr Leu Phe Ala Lys Tyr His Ala Thr Asp Cys Asn		

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1810	1815	1820
Ile Lys Leu Pro Phe	Phe Val Arg Ser Val	Ala Thr Phe Ile Met Gln
1825	1830	1835
Gly Ser Lys Leu Ser	Gly Ser Glu Cys Tyr	Ile Leu Leu Thr Leu Gly
1845	1850	1855
His His Asn Asn Leu	Pro Cys His Gly Glu	Ile Gln Asn Ser Lys Met
1860	1865	1870
Arg Ile Ala Val Cys	Asn Asp Phe His Ala	Ser Lys Lys Leu Asp Asn
1875	1880	1885
Lys Ser Ile Glu Ala	Asn Cys Lys Ser Leu	Leu Ser Gly Leu Arg Ile
1890	1895	1900
Pro Ile Asn Lys Lys	Glu Leu Asn Arg Gln	Lys Lys Leu Leu Thr Leu
1905	1910	1915
Gln Ser Asn His Ser	Ser Ile Ala Thr Val	Gly Gly Ser Lys Ile Ile
1925	1930	1935
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1940	1945	1950
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1955	1960	1965
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Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
 65          70          75          80
Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
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Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Val Glu Val Arg Gln
100          105          110
Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
115          120          125
Leu Val Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
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Leu Ile Ile Asp Leu Ser Ala Gly Ala Glu Asn Asp Ser Ser Tyr Ala
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Gly Tyr Ile Asp Asp Asn Gln Ser Ile Thr Lys Ala Ala Ala Cys Tyr
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<400> 341
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1 5 10 15
Arg Gly Ser Glu Cys Lys Phe Asn His Asn Tyr Trp Ser Trp Pro Asp
20 25 30
Arg Tyr Leu Leu Leu Arg Ser Asn Tyr Leu Leu Asn Gln Leu Leu Arg
35 40 45
Asn Thr Asp Lys Ala Asp Gly Leu Ser Ile Ile Ser Gly Ala Gly Arg
50 55 60
Glu Asp Arg Thr Gln Asp Phe Val Leu Gly Ser Thr Asn Val Val Gln
65 70 75 80
Gly Tyr Ile Asp Asn Asn Gln Gly Ile Thr Lys Ala Ala Cys Tyr
85 90 95
Ser Leu His Asn Ile Ile Lys Gln Leu Gln Glu Ile Glu Val Arg Gln
100 105 110
Ala Arg Asp Asn Lys Leu Ser Asp Ser Lys His Val Ala Leu His Asn
115 120 125
Leu Ile Leu Ser Tyr Met Glu Met Ser Lys Thr Pro Ala Ser Leu Ile
130 135 140
Asn Asn Leu Lys Lys Leu Pro Arg Glu Lys Leu Lys Lys Leu Ala Lys
145 150 155 160
Leu Ile Ile Asp Leu Ser Ala Gly Thr Asp Asn Asp Ser Ser Tyr Ala
165 170 175
Leu Gln Asp Ser Glu Ser Thr Asn Gln Val Gln
180 185

<210> 342
<211> 564
<212> DNA
<213> human metapneumo virus

<400> 342
atgtctcgca aggctccgtg caaatatgaa gtgcggggca aatgcaatag aggaagtgaag 60
tgcaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaatt 120
tatttattaa atcaactttt aaggaacact gatagagctg atggcttatc aataatatca 180
ggagcaggca gagaagatag gacacaagat tttgtcctag gttccaccaa tgtggttcaa 240
ggttatattg atgataacca aagcataaca aaagctgcag cctgttacag tctacataat 300
ataatcaaac aactacaaga agttgaagtt aggcaggcta gagataacaa actatctgac 360
agcaaacatg tagcacttca caacttagtc ctatcttata tggagatgag caaaactcct 420
gcatctttaa tcaacaatct caagagactg ccgagagaga aactgaaaaa attagcaaag 480
ctcataattg acttatcagc aggtgctgaa aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgca gtga 564

<210> 343
<211> 564
<212> DNA
<213> human metapneumo virus

<400> 343
atgtctcgca aggctccatg caaatatgaa gtgcggggca aatgcaacag aggaagtgaag 60
tgtaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120

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```
tatctattaa atcagctttt aaggaacact gatagagctg atggcctatc aataatatca 180
ggcgacaggca gagaagacag aacgcaagat tttgttctag gttccaccaa tgtggttcaa 240
ggttatattg atgataacca aagcataaca aaagctgcag cctgctacag tctacacaac 300
ataatcaagc aactacaaga agttgaagtt aggcaggcta gagatagcaa actatctgac 360
agcaagcatg tggcaactcca taacttaatc ttatcttaca tggagatgag caaaactccc 420
gcatctttaa tcaacaatct taaaagactg ccgagagaaa aactgaaaaa attagcaaa 480
ctgataattg acttatcagc aggcgctgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtga 564
```

<210> 344

<211> 564

<212> DNA

<213> human metapneumo virus

<400> 344

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atgtctcgta aggcctccatg caaatatgaa gtgcggggca aatgcaacag agggagtgat 60
tgcaaatcca atcacaatta ctggagtggg cctgatagat atttattgtt aagatcaa 120
tatctcttaa atcagctttt aagaaacaca gataaggctg atggtttgtc aataatatca 180
ggagcaggta gagaagatag aactcaagac tttgttcttg gttctactaa tgtggttcaa 240
gggtacattg atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgat 360
agcaaacatg tggcgctcca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatctctaa tcaacaacct aaagaaacta ccaagggaaa aactgaagaa attagcaaga 480
ttaataattg atttatcagc aggaactgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtaa 564
```

<210> 345

<211> 564

<212> DNA

<213> human metapneumo virus

<400> 345

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atgtctcgca aagctccatg caaatatgaa gtacggggca agtgcaacag gggaagtgag 60
tgcaaatcca accacaatta ctggagctgg cctgatagggt atttattgtt aagatcaa 120
tatctcttga atcagctttt aagaaacact gataaggctg atggtttgtc aataatatca 180
ggagcaggta gagaagatag gactcaagac tttgttcttg gttctactaa tgtggttcaa 240
gggtacattg ataacaatca aggaataaca aaggctgcag cttgctatag tctacataac 300
ataataaaac agctacaaga aatagaagta agacaggcta gagataataa gctttctgac 360
agcaaacatg tggcacttca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatccctga ttaataacct aaagaaacta ccaagagaaa aactgaagaa attagcgaaa 480
ttaataattg atttatcagc aggaactgat aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtaa 564
```

<210> 346

<211> 71

<212> PRT

<213> human metapneumo virus

<400> 346

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Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Asp Met Ile
20 25 30
Trp Thr His Lys Asp Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Ala Tyr Leu Ser
65 70
```

<210> 347

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<211> 71
<212> PRT
<213> human metapneumo virus

<400> 347
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Glu His Gly Pro Val Phe Ile Thr Ile Glu Val Asp Glu Met Ile
20 25 30
Trp Thr Gln Lys Glu Leu Lys Glu Ala Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Asn Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Ala Tyr Leu Ser
65 70

<210> 348
<211> 71
<212> PRT
<213> human metapneumo virus

<400> 348
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
20 25 30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Thr Tyr Leu Ser
65 70

<210> 349
<211> 71
<212> PRT
<213> human metapneumo virus

<400> 349
Met Thr Leu His Met Pro Cys Lys Thr Val Lys Ala Leu Ile Lys Cys
1 5 10 15
Ser Lys His Gly Pro Lys Phe Ile Thr Ile Glu Ala Asp Asp Met Ile
20 25 30
Trp Thr His Lys Glu Leu Lys Glu Thr Leu Ser Asp Gly Ile Val Lys
35 40 45
Ser His Thr Asn Ile Tyr Ser Cys Tyr Leu Glu Asn Ile Glu Ile Ile
50 55 60
Tyr Val Lys Ala Tyr Leu Ser
65 70

<210> 350
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 350
atgactcttc atatgccttg caagacagtg aaagcactaa tcaagtgcag tgagcatggt 60
ccagttttca ttactataga gggtgatgac atgatatgga ctcacaagga cttaaaagaa 120
gcttttatctg atgggatagt gaagtctcat actaacattt acaattgtta tttagaaaaac 180

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atagaaatta tatatgtcaa ggcttactta agttag 216

<210> 351
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 351
atgactcttc atatgccctg caagacagtg aaagcactaa tcaagtgcag tgagcatggt 60
cctgttttca ttactataga ggttgatgaa atgatatgga ctcaaaaaga attaaaagaa 120
gctttgtccg atgggatagt gaagtctcac accaacattt acaattgtta tttagaaaac 180
atagaaatta tatatgtcaa ggcttactta agttag 216

<210> 352
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 352
atgactcttc atatgccctg caagacagtg aaagcactaa tcaagtgcag taaacatggt 60
cccaaattca ttaccataga ggcagatgat atgatatgga ctcaaaaaga attaaaagaa 120
acactgtctg atgggatagt aaaatcacac accaatattt atagttgtta cttagaaaaa 180
atagaaataa tatatgttaa aacttactta agttag 216

<210> 353
<211> 216
<212> DNA
<213> human metapneumo virus

<400> 353
atgactcttc atatgccctg caagacagtg aaagcactaa tcaagtgcag taagcatggt 60
cccaaattca ttaccataga ggcagatgat atgatatgga cacacaaaga attaaaggag 120
acactgtctg atgggatagt aaaatcacac accaatattt acagttgtta tttagaaaaa 180
atagaaataa tatatgttaa agcttactta agttag 216

<210> 354
<211> 727
<212> DNA
<213> human metapneumo virus

<400> 354
atgtctcgca aggctccgtg caaatatgaa gtgcggggca aatgcaatag aggaagtgag 60
tgcaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaat 120
tatttattaa atcaactttt aaggaacact gatagagctg atggcttatc aataatatca 180
ggagcaggca gagaagatag gacacaagat tttgtcctag gttccaccaa tgtggttcaa 240
ggtttatattg atgataacca aagcataaca aaagctgcag cctgttacag tctacataat 300
ataatcaaac aactacaaga agttgaagtt aggcaggcta gagataacaa actatctgac 360
agcaaacatg tagcacttca caacttagtc ctatcttata tggagatgag caaaactcct 420
gcactctttaa tcaacaatct caagagactg ccgagagaga aactgaaaaa attagcaaag 480
ctcataattg acttatcagc aggtgctgaa aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtgagcatgg tccagttttc attactatag aggttgatga 600
catgatatgg actcacaagg acttaaaaaga agctttatct gatgggatag tgaagtctca 660
tactaacatt tacaattgtt atttagaaaa catagaaatt atatatgtca aggcttactt 720
aagtttag 727

<210> 355
<211> 727
<212> DNA
<213> human metapneumo virus

<400> 355
atgtctcgca aggctccatg caaatatgaa gtgcggggca aatgcaacag aggaagtgag 60

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tgtaagttta accacaatta ctggagttgg ccagatagat acttattaat aagatcaaac 120
tatctattaa atcagctttt aaggaacact gatagagctg atggcctatc aataatatca 180
ggcgaggca gagaagacag aacgcaagat tttgttctag gttccaccaa tgtggttcaa 240
ggttatattg atgataacca aagcataaca aaagctgcag cctgctacag tctacacaac 300
ataatcaagc aactacaaga agttgaagtt aggcaggcta gagatagcaa actatctgac 360
agcaagcatg tggcactcca taacttaatc ttatcttaca tggagatgag caaaactccc 420
gcatctttta tcaacaatct taaaagactg ccgagagaaa aactgaaaaa attagcaaac 480
ctgataattg acttatcagc aggcgctgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtgagcatgg tctgttttct attactatag aggttgatga 600
aatgatattg actcaaaaag aattaaaaga agctttgtcc gatgggatag tgaagtctca 660
caccaacatt tacaattggt atttagaaaa catagaaatt atatattgtca aggccttactt 720
aagttag 727

```

<210> 356

<211> 727

<212> DNA

<213> human metapneumo virus

<400> 356

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atgtctcgtg aggcctccatg caaatatgaa gtgcggggca aatgcaacag agggagtgat 60
tgcaaatcca atcacaatta ctggagttgg cctgatagat atttattgtt aagatcaaac 120
tatctcttaa atcagctttt aagaacacac gataaggctg atggtttgtc aataatatca 180
ggagcaggta gagaagatag aactcaagac tttgttcttg gttctactaa tgtggttcaa 240
gggtacattg atgacaacca aggaataacc aaggctgcag cttgctatag tctacacaac 300
ataatcaagc aactacaaga aacagaagta agacaggcta gagacaacaa gctttctgat 360
agcaaacatg tggcgctcca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatctctaa tcaacaacct aaagaaacta ccaagggaaa aactgaagaa attagcaaga 480
ttaataattg atttatcagc aggaactgac aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtaaacatgg tcccaaattc attaccatag aggcagatga 600
tatgatattg actcacaag aattaaaaga aacactgtct gatgggatag taaaatcaca 660
caccaatatt tatagttggt acttagaaaa tatagaaata atatattgta aaacttactt 720
aagttag 727

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<210> 357

<211> 727

<212> DNA

<213> human metapneumo virus

<400> 357

```

atgtctcgcg aagctccatg caaatatgaa gtacggggca agtgcaacag gggaagtgat 60
tgcaaatcca accacaatta ctggagctgg cctgataggt atttattgtt aagatcaaac 120
tatctcttga atcagctttt aagaacact gataaggctg atggtttgtc aataatatca 180
ggagcaggta gagaagatag gactcaagac tttgttcttg gttctactaa tgtggttcaa 240
gggtacattg ataacaatca aggaataaca aaggctgcag cttgctatag tctacataac 300
ataataaaaac agctacaaga aatagaagta agacaggcta gagataataa gctttctgac 360
agcaaacatg tggcacttca caacttgata ttatcctata tggagatgag caaaactcct 420
gcatccctga ttaataacct aaagaaacta ccaagagaaa aactgaagaa attagcgaaa 480
ttaataattg atttatcagc aggaactgat aatgactctt catatgcctt gcaagacagt 540
gaaagcacta atcaagtgcg gtaagcatgg tcccaaattc attaccatag aggcagatga 600
tatgatattg acacacaaag aattaaaaga gacactgtct gatgggatag taaaatcaca 660
caccaatatt tacagttggt atttagaaaa tatagaaata atatattgta aagcttactt 720
aagttag 727

```

<210> 358

<211> 254

<212> PRT

<213> human metapneumo virus

<400> 358

```

Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
 1           5           10          15
Ala Val Gln Val Asp Leu Ile Glu Lys Asp Leu Leu Pro Ala Ser Leu

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                20                25                30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
      35      40      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
      50      55      60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65      70      75      80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
      85      90      95
Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val
      100      105      110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
      115      120      125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
      130      135      140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile
145      150      155      160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
      165      170      175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
      180      185      190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
      195      200      205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
      210      215      220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys
225      230      235      240
Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
      245      250

```

<210> 359
 <211> 254
 <212> PRT
 <213> human metapneumo virus

```

<400> 359
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
1      5      10      15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
      20      25      30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
      35      40      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
      50      55      60
Gln Ser Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
65      70      75      80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
      85      90      95
Asp Glu Tyr Ser Lys Leu Glu Phe Asp Lys Leu Thr Val Cys Glu Val
      100      105      110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
      115      120      125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
      130      135      140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Thr Pro Val Thr Ile
145      150      155      160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
      165      170      175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
      180      185      190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn

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      195      200      205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
  210      215      220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Lys Ile Cys Lys
  225      230      235      240
Thr Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Ser
      245      250

```

```

<210> 360
<211> 254
<212> PRT
<213> human metapneumo virus

```

```

<400> 360
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
  1      5      10      15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
      20      25      30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
      35      40      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser
      50      55      60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala
      65      70      75      80
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu
      85      90      95
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val
      100      105      110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys
      115      120      125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile
      130      135      140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Ile Pro Val Thr Ile
      145      150      155      160
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr
      165      170      175
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala
      180      185      190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn
      195      200      205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val
      210      215      220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys
      225      230      235      240
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg
      245      250

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```

<210> 361
<211> 254
<212> PRT
<213> human metapneumo virus

```

```

<400> 361
Met Glu Ser Tyr Leu Val Asp Thr Tyr Gln Gly Ile Pro Tyr Thr Ala
  1      5      10      15
Ala Val Gln Val Asp Leu Val Glu Lys Asp Leu Leu Pro Ala Ser Leu
      20      25      30
Thr Ile Trp Phe Pro Leu Phe Gln Ala Asn Thr Pro Pro Ala Val Leu
      35      40      45
Leu Asp Gln Leu Lys Thr Leu Thr Ile Thr Thr Leu Tyr Ala Ala Ser

```

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50	55	60
Gln Asn Gly Pro Ile Leu Lys Val Asn Ala Ser Ala Gln Gly Ala Ala		
65	70	75
Met Ser Val Leu Pro Lys Lys Phe Glu Val Asn Ala Thr Val Ala Leu		80
	85	90
Asp Glu Tyr Ser Lys Leu Asp Phe Asp Lys Leu Thr Val Cys Asp Val		95
100	105	110
Lys Thr Val Tyr Leu Thr Thr Met Lys Pro Tyr Gly Met Val Ser Lys		115
115	120	125
Phe Val Ser Ser Ala Lys Ser Val Gly Lys Lys Thr His Asp Leu Ile		130
130	135	140
Ala Leu Cys Asp Phe Met Asp Leu Glu Lys Asn Ile Pro Val Thr Ile		145
145	150	155
Pro Ala Phe Ile Lys Ser Val Ser Ile Lys Glu Ser Glu Ser Ala Thr		160
	165	170
Val Glu Ala Ala Ile Ser Ser Glu Ala Asp Gln Ala Leu Thr Gln Ala		175
180	185	190
Lys Ile Ala Pro Tyr Ala Gly Leu Ile Met Ile Met Thr Met Asn Asn		195
195	200	205
Pro Lys Gly Ile Phe Lys Lys Leu Gly Ala Gly Thr Gln Val Ile Val		210
210	215	220
Glu Leu Gly Ala Tyr Val Gln Ala Glu Ser Ile Ser Arg Ile Cys Lys		225
225	230	235
Ser Trp Ser His Gln Gly Thr Arg Tyr Val Leu Lys Ser Arg		240
	245	250

<210> 362
<211> 765
<212> DNA
<213> human metapneumo virus

```

<400> 362
atggagtcct acctagtaga cacctatcaa ggcattccctt acacagcagc tgttcaagtt 60
gatctaataag aaaaggacct gttacctgca agcctaacaa tatgggttccc ttgttttcag 120
gccaacacac caccagcagt gctgctcgat cagctaaaaa cctgacaat aaccactctg 180
tatgctgcat cacaaaatgg tccaatactc aaagtgaatg catcagccca aggtgcagca 240
atgtctgtac ttcccaaaaa atttgaagtc aatgcgactg tagcactcga tgaatatagc 300
aaactggaat ttgacaaact cacagtctgt gaagtaaaaa cagtttactt aacaaccatg 360
aaaccatacg ggatgggtatc aaaattttgt agctcagcca aatcagtttg caaaaaaaca 420
catgatctaa tcgcactatg tgattttatg gatctagaaa agaacacacc tgttacaata 480
ccagcattca tcaaatacgt ttcaatcaaa gagagtgaat cagctactgt tgaagctgct 540
ataagcagtg aagcagacca agctctaaca caggccaaaa ttgcacctta tgcgggatta 600
attatgatca tgactatgaa caatcccaaa ggcataattca aaaagcttgg agctgggact 660
caagtcatag tagaactagg agcatatgtc caggctgaaa gcataagcaa aatatgcaag 720
acttgagacc atcaagggac aagatatgtc ttgaagtcca gataa 765

```

<210> 363
<211> 765
<212> DNA
<213> human metapneumo virus

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<400> 363
atggagtcct atctggtaga caattatcaa ggcattccctt acacagcagc tgttcaagtt 60
gatctagtag aaaaggacct gttacctgca agcctaacaa tatgggttccc ctgttttcag 120
gccaatacac caccagcagt tctgcttgat cagctaaaga ctctgactat aactactctg 180
tatgctgcat cacaaagtgg tccaatacta aaagtgaatg catcagccca ggtgcagca 240
atgtctgtac ttcccaaaaa gtttgaagtc aatgcgactg tagcacttga cgaatatagc 300
aaattagaat ttgacaaact tacagtctgt gaagtaaaaa cagtttactt aacaaccatg 360
aaaccatatg ggatgggtatc aaagtttgtg agctcggcca aatcagtttg caaaaaaaca 420
catgatctaa tcgcattatg tgattttatg gatctagaaa agaacacacc agttacaata 480
ccagcattta tcaaatacgt ttctatcaag gagagtgaat cagccactgt tgaagctgca 540

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```
ataagcagtg aagcagacca agctctaaca caagccaaaa ttgcacctta tgcgggactg 600
atcatgatta tgaccatgaa caatcccaaa ggcatattca agaagcttgg agctgggacc 660
caagttatag tagaactagg agcatatgtc caggctgaaa gcataagtaa aatatgcaag 720
acttgagacc atcaaggaac aagatatgtg ctgaagtcca gtttaa 765
```

<210> 364

<211> 765

<212> DNA

<213> human metapneumo virus

<400> 364

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atggagtcct atctagtaga cacttatcaa ggcattccat atacagctgc tgttcaagtt 60
gacctggtag aaaaagattt actgccagca agtttgacaa tatggtttcc tttatttcag 120
gccaacacac caccagcagt tctgcttgat cagctaaaaa ccttgacaat aacaactctg 180
tatgctgcat cacagaatgg tccaatactc aaggtaaatg catctgcccc aggtgctgcc 240
atgtctgtac ttcccaaaaa attcgaggta aatgcaactg tagcacttga tgaatacagt 300
aaacttgatt ttgacaagct gacggtctgc gatgttaaaa cagtttattt gacaactatg 360
aaaccgtacg ggatggtgtc aaaatttgtg agttcagcca aatcagttgg caaaaagaca 420
catgatctaa ttgcactatg tgacttcatg gacctagaga aaaatatacc tgtgacaata 480
ccagcattca taaagtcagt ttcaatcaaa gagagtgaat cagccactgt tgaagctgca 540
ataagcagcg aagccgacca agccttgaca caagccaaga ttgcgccta tgcaggacta 600
attatgatca tgaccatgaa caatccaaaa ggtatattca agaaactagg ggctggaaca 660
caagtgatag tagagctggg ggcatatgtt caggctgaga gcatacagtag gatctgcaag 720
agctggagtc accaaggaac aagatacgtg ctaaaatcca gataa 765
```

<210> 365

<211> 765

<212> DNA

<213> human metapneumo virus

<400> 365

```
atggagtcct atctagtga cacttatcaa ggcattccct acacagctgc tgttcaagtt 60
gatctggtag aaaaagactt actaccagca agtttgacaa tatggtttcc tctattccaa 120
gccaacacac caccagcggg tttgctcgat cagctaaaaa ccttgactat aacaactctg 180
tatgctgcat cacagaatgg tccaatactc aaagtaaatg catcagctca ggggtgctgct 240
atgtctgtac ttcccaaaaa attcgaagta aatgcaactg tggcacttga tgaatacagc 300
aaacttgact ttgacaagtt aacggtttgc gatgttaaaa cagtttattt gacaaccatg 360
aagccatatg ggatggtgtc aaaatttgtg agttcagcca aatcagttgg caaaaagaca 420
catgatctaa ttgcactgtg tgacttcatg gacctagaga aaaatatacc tgtgacaata 480
ccagcattca taaagtcagt ttcaatcaaa gagagtgaat cagccactgt tgaagctgca 540
ataagcagtg aggccgacca agcattaaca caagccaaaa ttgcacccta tgcaggacta 600
atcatgatca tgaccatgaa caatccaaaa ggtatattca agaaactagg agctggaaca 660
caagtgatag tagagctagg ggcatatgtt caagccgaga gcatacagcag gatctgcaag 720
agctggagtc accaaggaac aagatatgta ctaaaatcca gataa 765
```

<210> 366

<211> 394

<212> PRT

<213> human metapneumo virus

<400> 366

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Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
  1           5           10           15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
  20           25           30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
  35           40           45
Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
  50           55           60
Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
  65           70           75           80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
```

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```

      85      90      95
Thr Tyr Ser Leu Gly Lys Ile Lys Asn Lys Gly Glu Asp Leu Gln
      100      105      110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
      115      120      125
Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
      130      135      140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
      145      150      155      160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
      165      170      175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
      180      185      190
Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
      195      200      205
Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr His Arg Ser Leu Phe
      210      215      220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
      225      230      235      240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
      245      250      255
Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Ile Met
      260      265      270
Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
      275      280      285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
      290      295      300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
      305      310      315      320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
      325      330      335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
      340      345      350
Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
      355      360      365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
      370      375      380
Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
      385      390

```

<210> 367

<211> 394

<212> PRT

<213> human metapneumo virus

<400> 367

```

Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
  1      5      10      15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
      20      25      30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
      35      40      45
Gly Glu Ile Leu Tyr Ala Lys His Ala Asp Tyr Lys Tyr Ala Ala Glu
      50      55      60
Ile Gly Ile Gln Tyr Ile Ser Thr Ala Leu Gly Ser Glu Arg Val Gln
      65      70      75      80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Arg
      85      90      95
Thr Tyr Ser Leu Gly Lys Val Lys Asn Asn Lys Gly Glu Asp Leu Gln
      100      105      110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp

```

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PCT/US03/05271

```

      115      120      125
Lys Glu Ala Arg Lys Thr Met Ala Thr Leu Leu Lys Glu Ser Ser Gly
130      135      140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
145      150      155      160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
      165      170      175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
180      185      190
Asp Ala Leu Lys Arg Tyr Pro Arg Met Asp Ile Pro Lys Ile Ala Arg
195      200      205
Ser Phe Tyr Asp Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
210      215      220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
225      230      235      240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
      245      250      255
Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
260      265      270
Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
275      280      285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
290      295      300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305      310      315      320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
      325      330      335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
340      345      350
Ser Tyr Ala Lys Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
355      360      365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
370      375      380
Val Ser Asp Asp Ser Gln Asn Asp Tyr Glu
385      390

```

```

<210> 368
<211> 394
<212> PRT
<213> human metapneumo virus

```

```

<400> 368
Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
1      5      10      15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
20      25      30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
35      40      45
Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu
50      55      60
Ile Gly Ile Gln Tyr Ile Cys Thr Ala Leu Gly Ser Glu Arg Val Gln
65      70      75      80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Lys
85      90      95
Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
100      105      110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Ile Glu Glu Ile Asp
115      120      125
Lys Glu Ala Arg Lys Thr Met Val Thr Leu Leu Lys Glu Ser Ser Gly
130      135      140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile

```

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```

145          150          155          160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
          165          170          175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser
          180          185          190
Asp Ala Leu Lys Arg Tyr Pro Arg Ile Asp Ile Pro Lys Ile Ala Arg
          195          200          205
Ser Phe Tyr Glu Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
          210          215          220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
225          230          235          240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
          245          250          255
Thr Leu Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
          260          265          270
Leu Gly His Val Ser Val Gln Ser Glu Leu Lys Gln Val Thr Glu Val
          275          280          285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
          290          295          300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305          310          315          320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
          325          330          335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
          340          345          350
Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
          355          360          365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
          370          375          380
Met Ser Gly Asp Asn Gln Asn Asp Tyr Glu
385          390

```

<210> 369
 <211> 394
 <212> PRT
 <213> human metapneumo virus

```

<400> 369
Met Ser Leu Gln Gly Ile His Leu Ser Asp Leu Ser Tyr Lys His Ala
  1          5          10          15
Ile Leu Lys Glu Ser Gln Tyr Thr Ile Lys Arg Asp Val Gly Thr Thr
          20          25          30
Thr Ala Val Thr Pro Ser Ser Leu Gln Gln Glu Ile Thr Leu Leu Cys
          35          40          45
Gly Glu Ile Leu Tyr Thr Lys His Thr Asp Tyr Lys Tyr Ala Ala Glu
          50          55          60
Ile Gly Ile Gln Tyr Ile Cys Thr Ala Leu Gly Ser Glu Arg Val Gln
65          70          75          80
Gln Ile Leu Arg Asn Ser Gly Ser Glu Val Gln Val Val Leu Thr Lys
          85          90          95
Thr Tyr Ser Leu Gly Lys Gly Lys Asn Ser Lys Gly Glu Glu Leu Gln
          100          105          110
Met Leu Asp Ile His Gly Val Glu Lys Ser Trp Val Glu Glu Ile Asp
          115          120          125
Lys Glu Ala Arg Lys Thr Met Val Thr Leu Leu Lys Glu Ser Ser Gly
          130          135          140
Asn Ile Pro Gln Asn Gln Arg Pro Ser Ala Pro Asp Thr Pro Ile Ile
145          150          155          160
Leu Leu Cys Val Gly Ala Leu Ile Phe Thr Lys Leu Ala Ser Thr Ile
          165          170          175
Glu Val Gly Leu Glu Thr Thr Val Arg Arg Ala Asn Arg Val Leu Ser

```

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```

                180                185                190
Asp Ala Leu Lys Arg Tyr Pro Arg Val Asp Ile Pro Lys Ile Ala Arg
                195                200                205
Ser Phe Tyr Glu Leu Phe Glu Gln Lys Val Tyr Tyr Arg Ser Leu Phe
                210                215                220
Ile Glu Tyr Gly Lys Ala Leu Gly Ser Ser Ser Thr Gly Ser Lys Ala
225                230                235                240
Glu Ser Leu Phe Val Asn Ile Phe Met Gln Ala Tyr Gly Ala Gly Gln
                245                250                255
Thr Met Leu Arg Trp Gly Val Ile Ala Arg Ser Ser Asn Asn Ile Met
                260                265                270
Leu Gly His Val Ser Val Gln Ala Glu Leu Lys Gln Val Thr Glu Val
                275                280                285
Tyr Asp Leu Val Arg Glu Met Gly Pro Glu Ser Gly Leu Leu His Leu
                290                295                300
Arg Gln Ser Pro Lys Ala Gly Leu Leu Ser Leu Ala Asn Cys Pro Asn
305                310                315                320
Phe Ala Ser Val Val Leu Gly Asn Ala Ser Gly Leu Gly Ile Ile Gly
                325                330                335
Met Tyr Arg Gly Arg Val Pro Asn Thr Glu Leu Phe Ser Ala Ala Glu
                340                345                350
Ser Tyr Ala Arg Ser Leu Lys Glu Ser Asn Lys Ile Asn Phe Ser Ser
                355                360                365
Leu Gly Leu Thr Asp Glu Glu Lys Glu Ala Ala Glu His Phe Leu Asn
                370                375                380
Met Ser Asp Asp Asn Gln Asp Asp Tyr Glu
385                390

```

<210> 370
 <211> 1185
 <212> DNA
 <213> human metapneumo virus

```

<400> 370
atgtctcttc aagggattca cctgagtgat ttatcatata agcatgctat attaaaagag 60
tctcagtaca caataaaaag agatgtgggt acaacaactg cagtgcacacc ctcattcattg 120
caacaagaaa taactactgt gtgtggagaa attctgtatg ctaaacatgc tgactacaaa 180
tatgtgcag aaataggaat acaatatatt agcacagctt taggatcaga gagagtgcag 240
cagattctga ggaactcagg cagtgaagtc caagtggctt taaccagaac gtactctctg 300
gggaaaatta aaaacaataa aggagaagat ttacagatgt tagacataca cggggtagag 360
aagagctggg tagaagagat agacaaagaa gcaaggaaaa caatggcaac cttgtctaag 420
gaatcatcag gtaatatccc acaaaatcag aggcctcag caccagacac acccataatc 480
ttattatgtg taggtgcctt aatattcact aaactagcat caaccataga agtgggacta 540
gagaccacag tcagaagggc taaccgtgta ctaagtgat cactcaagag ataccctaga 600
atggacatac caaagattgc cagatccttc tatgacttat ttgaacaaaa agtgtatcac 660
agaagtttgt tcattgagta tggcaaagca ttaggctcat catctacagg cagcaaagca 720
gaaagtctat ttgttaatat attcatgcaa gcttatgggg cgggtcaaac aatgctaagg 780
tgggggggtc ttgccaggtc atccaacaat ataatgttag gacatgtatc cgtccaagct 840
gagttaaaac aggtcacaga agtctatgac ttggtgagag aaatgggccc tgaatctgga 900
cttctacatt taaggcaaag cccaaaagct ggactgttat cactagccaa ctgtcccaac 960
tttgcaagtg ttgttctcgg aaatgcctca ggcttaggca taatcggtat gtatcgaggg 1020
agagtaccaa acacagaatt attttcagca gctgaaagtt atgccaaaag tttgaaagaa 1080
agcaataaaa taaatttctc ttcattagga cttacagatg aagagaaaag ggctgcagaa 1140
catttcttaa atgtgagtga cgacagtcaa aatgattatg agtaa 1185

```

<210> 371
 <211> 1185
 <212> DNA
 <213> human metapneumo virus

<400> 371

WO 03/072719

PCT/US03/05271

```

atgtctcttc aagggattca cctgagtgat ctatcatata agcatgctat attaaaagag 60
tctcagtata caataaagag agatgtaggc acaacaaccg cagtgcacac tcatcattg 120
caacaagaaa taacactatt gtgtggagaa attctatatg ctaagcatgc tgattacaaa 180
tatgctgcag aaataggaat acaatatatt agcacagctc taggatcaga gagagtacag 240
cagattctaa gaaactcagg tagtgaagtc caagtgggtt taaccagaac gtactccttg 300
gggaaagtta aaaacaacaa aggagaagat ttacagatgt tagacataca cggagtagag 360
aaaagctggg tggaagagat agacaaagaa gcaagaaaaa caatggcaac tttgcttaaa 420
gaatcatcag gcaatattcc acaaaatcag aggccttcag caccagacac acccataatc 480
ttattatgtg taggtgcctt aatatttacc aaactagcat caactataga agtgggatta 540
gagaccacag tcagaagagc taaccgtgta ctaagtgatg cactcaaaag ataccctagg 600
atggacatac caaaaatcgc tagatctttc tatgacttat ttgaacaaaa agtgatttac 660
agaagtttgt tcattgagta tggcaaagca tttaggtcat cctctacagg cagcaaagca 720
gaaagtttat tcgttaatat attcatgcaa gcttacggtg ctggtcaaac aatgctgagg 780
tggggagtca ttgccaggtc atctaacaat ataatggttag gacatgtatc tgttcaagct 840
gagttaaaac aagtcacaga agtctatgac ctggtgagag aaatgggccc tgaatctggg 900
ctcctacatt taaggcaaaag cccaaaagct ggactgttat cactagccaa ttgtcccaac 960
tttgctagtg ttgttctcgg caatgcctca ggcttaggca taataggtat gtatcgcggg 1020
agagtgcacaa acacagaact attttcagca gcagaaaagct atgccaaagag tttgaaagaa 1080
agcaataaaaa ttaacttttc ttcattagga ctcacagatg aagaaaaaga ggctgcagaa 1140
cacttcttaa atgtgagtga cgacagtcaa aatgattatg agtaa 1185

```

<210> 372

<211> 1185

<212> DNA

<213> human metapneumo virus

<400> 372

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atgtctcttc aagggattca cctaagtgat ctatcatata aacatgctat attaaaagag 60
tctcaatata caataaaaaag agatgtaggc accacaactg cagtgcacac ttcattcatta 120
caacaagaaa taacactttt gtgtgggagaa atactttaca ctaaacacac tgattacaaa 180
tatgctgctg agataggaat acaatatatt tgcacagctc taggatcaga aagagtacaa 240
cagattttga gaaactcagg tagtgaagtt caggtggttc taaccaaaac atactcctta 300
gggaaaggca aaaacagtaa aggggaagag ctgcagatgt tagatataca tggagtgga 360
aagagttgga tagaagaaat agacaaagag gcaagaaaaga caatggtaac tttgcttaag 420
gaatcatcag gtaacatccc acaaaaccag agaccttcag caccagacac accaataatt 480
ttattatgtg taggtgcctt aatattcact aaactagcat caacaataga agttggatta 540
gagactacag ttagaagagc taatagagtg ctaagtgatg cactcaaaag atacccaagg 600
atagatatac caaagattgc tagatctttt ttgaactat ttgaacaaaa agtggtactac 660
agaagtttat tcattgagta cggaaaagct tttaggtcat cttcaacagg aagcaaaagca 720
gaaagtttgt ttgtaaatat atttatgcaa gcttatggag ctggccaaac actgctaagg 780
tggggtgtca ttgccagatc atccaacaac ataatgctag ggcatgtatc tgtgcaatct 840
gaattgaagc aagttacaga ggtttatgac ttggtgagag aaatgggtcc tgaatctggg 900
cttttacatc taagacaaaag tccaaaggca gggctgttat cattggccaa ttgccccaat 960
tttgctagtg ttgttcttgg caatgcttca ggtctaggca taatcggaat gtacagaggg 1020
agagtaccaa acacagagct attttctgca gcagaaaagtt atgccagaag cttaaaagaa 1080
agcaataaaaa tcaacttctc ttctgttaggg cttacagatg aagaaaaaga agctgcagaa 1140
cacttcttaa acatgagtgg tgacaatcaa aatgattatg agtaa 1185

```

<210> 373

<211> 1185

<212> DNA

<213> human metapneumo virus

<400> 373

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atgtctcttc aagggattca cctaagtgat ctgtcatata aacatgctat attaaaagag 60
tctcaatata caataaaaaag agatgtaggc accacaactg cagtgcacac ttcattcattg 120
cagcaagaga taacactttt gtgtggagag attctttaca ctaaacatac tgattacaaa 180
tatgctgcag agatagggat acaatatatt tgcacagctc taggatcaga aagagtacaa 240
cagattttta gaaattcagg tagtgagggt caggtggttc taaccaagac atactcttta 300
gggaaaggta aaaatagtaa aggggaagag tgcacaaatg tagatataca tggagtgga 360
aagagttggg tagaagaaat agacaaagag gcaagaaaaa caatgggtgac tttgctaaag 420
gaatcatcag gcaacatccc acaaaaccag aggccttcag caccagacac accaataatt 480

```


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```

ttattgtgtg taggtgcttt aatattcact aaactagcat caacaataga agttggacta 540
gagactacag ttagaagggc taacagagtg ttaagtgatg cgctcaaaag ataccctagg 600
gtagatatac caaagattgc tagatctttt tatgaactat ttgagcagaa agtgtattac 660
aggagtctat tcattgagta tgggaaagct ttaggctcat cttcaacagg aagcaaagca 720
gaaagtttgt ttgtaaatat atttatgcaa gcttatggag ccggtcagac aatgctaagg 780
tgggggtgtca ttgccagatc atctaacaac ataatgctag ggcatgtatc tgtgcaagct 840
gaattgaaac aagttacaga ggtttatgat ttggttaagag aaatgggtcc tgaatctggg 900
cttttacatc taagacaaaag tccaaaggca ggactgttat cgttgggctaa ttgccccaat 960
tttgctagtg ttgttcttgg taatgcttca ggtctaggta taatcggaat gtacagggga 1020
agagtgccaa acacagagct attttctgca gcagaaagtt atgccagaag cttaaaagaa 1080
agcaacaaaa tcaacttctc ctcattaggg ctcacagacg aagaaaaaga agctgcagaa 1140
cacttcttaa acatgagtga tgacaatcaa gatgattatg agtaa 1185

```

<210> 374

<211> 294

<212> PRT

<213> human metapneumo virus

<400> 374

```

Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
 1          5          10          15
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Gly His
 20          25          30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu
 35          40          45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Ala Lys Pro Thr Ile Pro
 50          55          60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Thr Lys Thr
 65          70          75          80
Glu Ile Lys Gln Ala Ile Lys Val Met Asp Pro Ile Glu Glu Glu Glu
 85          90          95
Ser Thr Glu Lys Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
100          105          110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Lys Val Ser Phe
115          120          125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
130          135          140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145          150          155          160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
165          170          175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
180          185          190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
195          200          205
Asp Ala Met Ile Gly Val Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys
210          215          220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Ser Gln
225          230          235          240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
245          250          255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
260          265          270
Glu Glu Glu Glu Pro Lys Asp Thr Gln Asp Asn Ser Gln Glu Asp Asp
275          280          285
Ile Tyr Gln Leu Ile Met
290

```

<210> 375

<211> 294

<212> PRT

WO 03/072719

PCT/US03/05271

<213> human metapneumo virus

<400> 375

```

Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
 1          5          10          15
Ala Lys Leu Ala Glu Ala Phe Gln Lys Ser Leu Arg Lys Pro Asn His
 20          25          30
Lys Arg Ser Gln Ser Ile Ile Gly Glu Lys Val Asn Thr Val Ser Glu
 35          40          45
Thr Leu Glu Leu Pro Thr Ile Ser Arg Pro Thr Lys Pro Thr Ile Leu
 50          55          60
Ser Glu Pro Lys Leu Ala Trp Thr Asp Lys Gly Gly Ala Ile Lys Thr
 65          70          75          80
Glu Ala Lys Gln Thr Ile Lys Val Met Asp Pro Ile Glu Glu Glu Glu
 85          90          95
Phe Thr Glu Lys Arg Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala
 100         105         110
Glu Lys Lys Leu Lys Pro Ser Thr Asn Thr Lys Lys Lys Val Ser Phe
 115         120         125
Thr Pro Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
 130         135         140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
 145         150         155         160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
 165         170         175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
 180         185         190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
 195         200         205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Asp Ile Ile Lys
 210         215         220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln
 225         230         235         240
Arg Thr Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
 245         250         255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
 260         265         270
Glu Glu Glu Glu Pro Lys Asp Thr Gln Glu Asn Asn Gln Glu Asp Asp
 275         280         285
Ile Tyr Gln Leu Ile Met
 290

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<210> 376

<211> 294

<212> PRT

<213> human metapneumo virus

<400> 376

```

Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
 1          5          10          15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Lys Ser Gly His
 20          25          30
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu
 35          40          45
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu
 50          55          60
Leu Glu Pro Lys Leu Ala Trp Ala Asp Asn Ser Gly Ile Thr Lys Ile
 65          70          75          80
Thr Glu Lys Pro Ala Thr Lys Thr Thr Asp Pro Val Glu Glu Glu Glu
 85          90          95
Phe Asn Glu Lys Lys Val Leu Pro Ser Ser Asp Gly Lys Thr Pro Ala

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          100          105          110
Glu Lys Lys Ser Lys Phe Ser Thr Ser Val Lys Lys Lys Val Ser Phe
          115          120          125
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
          130          135          140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145          150          155          160
Thr Phe Glu Glu Lys Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
          165          170          175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
          180          185          190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
          195          200          205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys
          210          215          220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln
225          230          235          240
Arg Ser Lys Ile Gly Asn Gly Ser Val Lys Leu Thr Glu Lys Ala Lys
          245          250          255
Glu Leu Asn Lys Ile Val Glu Asp Glu Ser Thr Ser Gly Glu Ser Glu
          260          265          270
Glu Glu Glu Glu Pro Lys Glu Thr Gln Asp Asn Asn Gln Gly Glu Asp
          275          280          285
Ile Tyr Gln Leu Ile Met
          290

```

<210> 377
 <211> 294
 <212> PRT
 <213> human metapneumo virus

```

<400> 377
Met Ser Phe Pro Glu Gly Lys Asp Ile Leu Phe Met Gly Asn Glu Ala
 1          5          10          15
Ala Lys Ile Ala Glu Ala Phe Gln Lys Ser Leu Lys Arg Ser Gly His
          20          25          30
Lys Arg Thr Gln Ser Ile Val Gly Glu Lys Val Asn Thr Ile Ser Glu
          35          40          45
Thr Leu Glu Leu Pro Thr Ile Ser Lys Pro Ala Arg Ser Ser Thr Leu
          50          55          60
Leu Glu Pro Lys Leu Ala Trp Ala Asp Ser Ser Gly Ala Thr Lys Thr
65          70          75          80
Thr Glu Lys Gln Thr Thr Lys Thr Thr Asp Pro Val Glu Glu Glu Glu
          85          90          95
Leu Asn Glu Lys Lys Val Ser Pro Ser Ser Asp Gly Lys Thr Pro Ala
          100          105          110
Glu Lys Lys Ser Lys Ser Pro Thr Asn Val Lys Lys Lys Val Ser Phe
          115          120          125
Thr Ser Asn Glu Pro Gly Lys Tyr Thr Lys Leu Glu Lys Asp Ala Leu
          130          135          140
Asp Leu Leu Ser Asp Asn Glu Glu Glu Asp Ala Glu Ser Ser Ile Leu
145          150          155          160
Thr Phe Glu Glu Arg Asp Thr Ser Ser Leu Ser Ile Glu Ala Arg Leu
          165          170          175
Glu Ser Ile Glu Glu Lys Leu Ser Met Ile Leu Gly Leu Leu Arg Thr
          180          185          190
Leu Asn Ile Ala Thr Ala Gly Pro Thr Ala Ala Arg Asp Gly Ile Arg
          195          200          205
Asp Ala Met Ile Gly Ile Arg Glu Glu Leu Ile Ala Glu Ile Ile Lys
          210          215          220
Glu Ala Lys Gly Lys Ala Ala Glu Met Met Glu Glu Glu Met Asn Gln

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225					230					235				240	
Arg	Ser	Lys	Ile	Gly	Asn	Gly	Ser	Val	Lys	Leu	Thr	Glu	Lys	Ala	Lys
				245					250					255	
Glu	Leu	Asn	Lys	Ile	Val	Glu	Asp	Glu	Ser	Thr	Ser	Gly	Glu	Ser	Glu
			260					265					270		
Glu	Glu	Glu	Glu	Pro	Lys	Glu	Thr	Gln	Asp	Asn	Asn	Gln	Gly	Glu	Asp
		275					280					285			
Ile	Tyr	Gln	Leu	Ile	Met										
	290														

<210> 378
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 378
atgtcattcc ctgaaggaaa agatattcct ttcattgggt atgaagcagc aaaattagca 60
gaagcttttc agaatcatt aagaaaacca ggtcataaaa gatctcaatc tattatagga 120
gaaaaagtga atactgtatc agaaacattg gaattaccta ctatcagtag acctgcaaaa 180
ccaaccatac cgtcagaacc aaagttagca tggacagata aaggtggggc aacccaaact 240
gaaataaagc aagcaatcaa agtcatggat cccattgaag aagaagagtc taccgagaag 300
aaggtgctac cctccagtga tgggaaaacc cctgcagaaa agaaactgaa accatcaact 360
aacaccaaaa agaaggtttc atttacacca aatgaaccag ggaaatatac aaagttggaa 420
aaagatgctc tagatttgct ctcagataat gaagaagaag atgcagaatc ttcaatctta 480
acctttgaag aaagagatac ttcattcatta agcattgagg ccagattgga atcaatagag 540
gagaaattaa gcatgatatt agggctatta agaactca acattgctac agcaggaccc 600
acagcagcaa gagatgggat cagagatgca atgattggcg taagagagga attaatagca 660
gacataataa aggaagctaa agggaaagca gcagaaatga tggaaagagga aatgagtcaa 720
cgatcaaaaa taggaaatgg tagtgtaaaa ttaacagaaa aagcaaaaaga gctcaacaaa 780
attgttgaag atgaaagcac aagtggagaa tccgaagaag aagaagaacc aaaagacaca 840
caagacaata gtcaagaaga tgacatttac cagttaatta tgtag 885

<210> 379
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 379
atgtcattcc ctgaaggaaa agatattcct ttcattgggt atgaagcagc aaaattggca 60
gaagcttttc aaaaatcatt aagaaaacct aatcataaaa gatctcaatc tattatagga 120
gaaaaagtga aactgtatc tgaacattg gaattaccta ctatcagtag acctacaaa 180
ccgaccatat tgtcagagcc gaagttagca tggacagaca aaggtggggc aatcaaaact 240
gaagcaaagc aaacaatcaa agttatggat cctattgaag aagaagagtt tactgagaaa 300
aggggtgctgc cctccagtga tgggaaaact cctgcagaaa agaagttgaa accatcaacc 360
aacactaaaa agaaggtctc atttacacca aatgaaccag gaaaatacac aaagttggag 420
aaagatgctc tagacttgct ttcagacaat gaagaagaag atgcagaatc ctcaatctta 480
accttcgaag aaagagatac ttcattcatta agcattgaag ccagactaga atcgattgag 540
gagaaattaa gcatgatatt agggctatta agaactca acattgctac agcaggaccc 600
acagcagcaa gagatgggat cagagatgca atgattggca taaggagagga actaatagca 660
gacataataa aagaagccaa gggaaaagca gcagaaatga tggaaagaaga aatgaaccag 720
cggacaaaaa taggaaacgg tagtgtaaaa ttaactgaaa aggcaaaagga gctcaacaaa 780
attgttgaag acgaaagcac aagtgggtgaa tccgaagaag aagaagaacc aaaagacaca 840
caggaaaata atcaagaaga tgacatttac cagttaatta tgtag 885

<210> 380
<211> 885
<212> DNA
<213> human metapneumo virus

<400> 380
atgtcattcc ctgaaggaaa ggatattctg ttcattgggt atgaagcagc aaaaatagcc 60

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gaagctttcc agaatcact gaaaaaatca ggtcacaaga gaactcaatc tattgtagg 120
gaaaaagtta acactatatac agaaactcta gaactaccta ccatcagcaa acctgcacga 180
tcattctacac tgctggaacc aaaattggca tgggcagaca acagcgggaat caccaaaatc 240
acagaaaaac cagcaaccaa aacaacagat cctgttgaag aagaggaatt caatgaaaag 300
aaagtgttac cttccagtga tgggaagact cctgcagaga aaaaatcaaa gttttcaacc 360
agtgtaaaaa agaaagtttc ctttacctca aatgaaccag ggaaatacac caaactagag 420
aaagatgccc tagatttgct ctcagacaat gaggaagaag acgcagaatc ctcaatccta 480
acttttgagg agaaagatac atcatcacta agcattgaag ctagactaga atctatagaa 540
gagaagttga gcatgatatt aggactgctt cgtacactta acattgcaac agcaggacca 600
acagctgcac gagatggaat tagggatgca atgattggta taagagaaga gctaatagca 660
gagataatta aggaagccaa gggaaaagca gctgaaatga tggagaaga gatgaatcaa 720
agatcaaaaa taggaaatgg cagtgtaaaa ctaaccgaga aggcaaaaaga gctcaacaaa 780
attgttgaag acgagagcac aagcggtgaa tcagaagaag aagaagaacc aaaagaaact 840
caggataaca atcaaggaga agatatattat cagttaatca tgtag 885

```

<210> 381

<211> 885

<212> DNA

<213> human metapneumo virus

<400> 381

```

atgtcattcc ctgaaggaaa agatatcctg ttcattgggt atgaagcagc aaaaatagca 60
gaagctttcc agaaatcact aaaaagatca ggtcacaaaa gaaccagtc tattgtagg 120
gaaaaagtta acactatatac agaaactcta gagctaccta ccatcagcaa acctgcacga 180
tcattctacac tgctagagcc aaaattggca tgggcagaca gcagcggagc caccaaaacc 240
acagaaaaac aaacaaccaa aacaacagat cctgttgaag aagaggaact caatgaaaag 300
aaggtatcac cttccagtga tgggaagact cctgcagaga aaaaatcaaa atctccaacc 360
aatgtaaaaa agaaagtttc cttcacatca aatgaaccag ggaaatatac taaactagaa 420
aaagatgccc tagatttgct ctcagacaat gaggaagaag acgcagagtc ctcaatccta 480
acctttgaag agagagacac atcatcacta agcattgagg ctagactaga atcaatagaa 540
gagaagctaa gcatgatatt aggactgctt cgtacactta acattgcaac agcaggacca 600
acggctgcaa gggatggaat cagagatgca atgattggta taagagaaga actaatagca 660
gaaataataa aagaagcaaa gggaaaagca gccgaaatga tggagaagga aatgaatcaa 720
aggtcaaaaa taggtaatgg cagtgtaaaa ctaaccgaga aggcaaaaaga acttaataaa 780
attgttgaag acgagagcac aagtggtgaa tcagaagaag aagaagaacc aaaagaaact 840
caggataaca atcaaggaga agatatctac cagttaatca tgtag 885

```

<210> 382

<211> 183

<212> PRT

<213> human metapneumo virus

<400> 382

```

Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys
1           5           10           15
Thr His Leu Lys Lys Ile Ile Lys Asp His Ser Gly Lys Val Leu Ile
20          25          30
Val Leu Lys Leu Ile Leu Ala Leu Thr Phe Leu Thr Val Thr Ile
35          40          45
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser
50          55          60
Lys Thr Glu Ser Asp Lys Lys Asp Ser Ser Ser Asn Thr Thr Ser Val
65          70          75          80
Thr Thr Lys Thr Thr Leu Asn His Asp Ile Thr Gln Tyr Phe Lys Ser
85          90          95
Leu Ile Gln Arg Tyr Thr Asn Ser Ala Ile Asn Ser Asp Thr Cys Trp
100         105         110
Lys Ile Asn Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu
115         120         125
Cys Phe Lys Ser Glu Asp Thr Lys Thr Asn Asn Cys Asp Lys Leu Thr
130         135         140
Asp Leu Cys Arg Asn Lys Pro Lys Pro Ala Val Gly Val Tyr His Ile

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145             150             155             160
Val Glu Cys His Cys Ile Tyr Thr Val Lys Trp Lys Cys Tyr His Tyr
              165             170             175
Pro Thr Asp Glu Thr Gln Ser
              180

```

<210> 383
 <211> 179
 <212> PRT
 <213> human metapneumo virus

```

<400> 383
Met Ile Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Lys Thr Cys
 1             5             10             15
Thr His Leu Lys Lys Ile Ile Lys Asp His Ser Gly Lys Val Leu Ile
 20             25             30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ile Thr Ile
 35             40             45
Thr Ile Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ile Cys Gln Ser
 50             55             60
Lys Thr Glu Ser Asp Lys Glu Asp Ser Pro Ser Asn Thr Thr Ser Val
 65             70             75             80
Thr Thr Lys Thr Thr Leu Asp His Asp Ile Thr Gln Tyr Phe Lys Arg
              85             90             95
Leu Ile Gln Arg Tyr Thr Asp Ser Val Ile Asn Lys Asp Thr Cys Trp
              100             105             110
Lys Ile Ser Arg Asn Gln Cys Thr Asn Ile Thr Thr Tyr Lys Phe Leu
              115             120             125
Cys Phe Lys Pro Glu Asp Ser Lys Ile Asn Ser Cys Asp Arg Leu Thr
 130             135             140
Asp Leu Cys Arg Asn Lys Ser Lys Ser Ala Ala Glu Ala Tyr His Thr
 145             150             155             160
Val Glu Cys His Cys Ile Tyr Thr Ile Glu Trp Lys Cys Tyr His His
              165             170             175
Pro Ile Asp

```

<210> 384
 <211> 177
 <212> PRT
 <213> human metapneumo virus

```

<400> 384
Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys
 1             5             10             15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Val Leu Ile
 20             25             30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Ala Thr Ile
 35             40             45
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Pro
 50             55             60
Lys Asn Glu Ser Asp Lys Lys Val Thr Lys Pro Asn Thr Thr Ser Thr
 65             70             75             80
Thr Ile Arg Pro Thr Pro Asp Pro Thr Val Val His His Leu Lys Arg
              85             90             95
Leu Ile Gln Arg His Thr Asn Ser Val Thr Lys Asp Ser Asp Thr Cys
              100             105             110
Trp Arg Ile His Lys Asn Gln Arg Thr Asn Ile Lys Ile Tyr Lys Phe
              115             120             125
Leu Cys Ser Gly Phe Thr Asn Ser Lys Gly Thr Asp Cys Glu Glu Pro

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```

      130      135      140
Thr Ala Leu Cys Asp Lys Lys Leu Lys Thr Ile Val Glu Lys His Arg
145      150      155      160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Gly Cys Leu His
      165      170      175
Pro

```

<210> 385
 <211> 177
 <212> PRT
 <213> human metapneumo virus

```

<400> 385
Met Lys Thr Leu Asp Val Ile Lys Ser Asp Gly Ser Ser Glu Thr Cys
  1      5      10      15
Asn Gln Leu Lys Lys Ile Ile Lys Lys His Ser Gly Lys Leu Leu Ile
      20      25      30
Ala Leu Lys Leu Ile Leu Ala Leu Leu Thr Phe Phe Thr Val Thr Ile
      35      40      45
Thr Val Asn Tyr Ile Lys Val Glu Asn Asn Leu Gln Ala Cys Gln Leu
      50      55      60
Lys Asn Glu Ser Asp Lys Lys Asp Thr Lys Leu Asn Thr Thr Ser Thr
      65      70      75      80
Thr Ile Arg Pro Ile Pro Asp Leu Asn Ala Val Gln Tyr Leu Lys Arg
      85      90      95
Leu Ile Gln Lys His Thr Asn Phe Val Ile Lys Asp Arg Asp Thr Cys
      100      105      110
Trp Arg Ile His Thr Asn Gln Cys Thr Asn Ile Lys Ile Tyr Lys Phe
      115      120      125
Leu Cys Phe Gly Phe Met Asn Ser Thr Asn Thr Asp Cys Glu Glu Leu
      130      135      140
Thr Val Leu Cys Asp Lys Lys Ser Lys Thr Met Thr Glu Lys His Arg
      145      150      155      160
Lys Ala Glu Cys His Cys Leu His Thr Thr Glu Trp Trp Cys Tyr Tyr
      165      170      175
Leu

```

<210> 386
 <211> 552
 <212> DNA
 <213> human metapneumo virus

```

<400> 386
atgataacat tagatgtcat taaaagtgat gggctcttcaa aaacatgtac tcacctcaaa 60
aaaataatta aagaccactc tggtaaagtg cttattgtac ttaagttaat attagcttta 120
ctaacatttc tcacagtaac aatcaccatc aattatataa aagtggaaaa caatctgcaa 180
atatgccagt caaaaactga atcagacaaa aaggactcat catcaaatac cacatcagtc 240
acaaccaaga ctactctaaa tcatgatatc acacagtatt ttaaaagttt gattcaaagg 300
tatacaaaact ctgcaataaaa cagtgcacaca tgctggaaaa taaacagaaa tcaatgcaca 360
aatataacaa catacaaat tttatgtttt aaatctgaag acacaaaaaac caacaattgt 420
gataaactga cagatttatg cagaaacaaa caaaaccag cagttggagt gtatcacata 480
gtagaatgcc attgtatata cacagttaaa tggaagtgct atcattaccc aaccgatgaa 540
accaatcct aa 552

```

<210> 387
 <211> 540
 <212> DNA
 <213> human metapneumo virus

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```
<400> 387
atgataacat tagatgtcat taaaagtgat gggctcttcaa aaacatgtac tcacctcaaa 60
aaaataatca aagaccattc tggtaaagtg cttattgcac ttaagttaat attagcttta 120
ctaacatttt tcacaataac aatcactata aattacataa aagtagaaaa caatctacaa 180
atatgccagt caaaaactga atcagacaaa gaagactcac catcaaatac cacatccgtc 240
acaaccaaga ctactctaga ccatgatata acacagtatt ttaaaagatt aattcaaagg 300
tatacagatt ctgtgataaa caaggacaca tgctggaaaa taagcagaaa tcaatgcaca 360
aatataacaa catataaatt tttatgcttt aaacctgagg actcaaaaat caacagttgt 420
gatagactga cagatctatg cagaaacaaa tcaaaatcag cagctgaagc atatcataca 480
gtagaatgcc attgcatata cacaattgag tggaaagtgc atcaccaccc aatagattaa 540
```

```
<210> 388
<211> 534
<212> DNA
<213> human metapneumo virus
```

```
<400> 388
atgaaaacat tagatgtcat aaaaagtgat ggatcctcag aaacgtgtaa tcaactcaaa 60
aaaataataa aaaaacactc aggtaaagtg cttattgcac taaaactgat attggcctta 120
ctgacatttt tcacagcaac aatcactgtc aactatataa aagtagaaaa caatttgcag 180
gcatgtcaac caaaaaatga atcagacaaa aaggtcacaa agccaaatac cacatcaaca 240
acaatcagac ccacaccoga tccaactgta gtacatcatt tgaaaaggct gattcagaga 300
cacaccaact ctgtcacaaa agacagcgat acttgttggg gaatacacaa gaatcaacgt 360
acaaatataa aaatatacaa gttcttatgc tctgggttca caaattcaaa aggtacagat 420
tgtgaggaac caacagccct atgcgacaaa aagttaaaaa ccatagtaga aaaacataga 480
aaagcagaat gtcactgtct acatacaacc gagtgggggt gccttcatcc ctaa 534
```

```
<210> 389
<211> 534
<212> DNA
<213> human metapneumo virus
```

```
<400> 389
atgaaaacat tagatgtcat aaaaagtgat ggatcctcag aaacatgtaa tcaactcaaa 60
aaaataataa aaaaacactc aggtaaattg cttattgcac taaaactgat attggcctta 120
ttgacgtttt tcacagtaac aattactgtt aactatataa aagtagaaaa caatttgcag 180
gcatgtcaat taaaaaatga atcagacaaa aaggacacaa agctaaatac cacatcaaca 240
acaatcagac ccattcctga tctaaatgca gtacagtact tgaaaaggct gattcagaaa 300
cacaccaact ttgtcataaa agacagagat acctgttggg gaatacacac gaatcaatgc 360
acaaatataa aaatataataa gttcttatgt ttctgggttta tgaattcaac aaatacagac 420
tgtgaagaac taacagtttt atgtgataaa aagtcaaaaa ccatgacaga aaaacatagg 480
aaagcagagt gtcactgtct acatacaacc gagtgggtgt gttattatct ttaa 534
```